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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Perfect score:
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# SUMMARIES

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KEYWORDS SOURCE	Un ·	known.				
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		Robin, G. Charle Boyce, T. Mark.,	12	<b>₩</b>	eville., Cl :,J.Graham.	ianos,C., Sm d Brownlie,J
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ocus	AR153438 1713 bp DNA linear PAT 08-AUG-2001	
DEFINITION	Sequence 1 from patent US 6235515.	
CCESSION	AR153438	
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EYWORDS		
OURCE	Unknown.	
ORGANISM	Unknown.	
	Unclassified.	
REFERENCE	1 (bases 1 to 1713)	
AUTHORS	Russell, R. Joyce., Newcomb, R. David., Campbell, P. Malcolm.,	
	Robin, G. Charlesde. Quetteville., Claudianos, C., Smyth, KA.,	
	Boyce, T. Mark., Oakeshott, J. Graham. and Brownlie, J. Colin.	
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                Unclassified.

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Russell, R. Joyce., Newcomb, R. David., Campbell, P. Malcolm., Robin, G. Charlesde. Quetteville., Claudianos, C., Smyth, K.-A., Boyce, T. Mark., Oakeshott, J. Graham. and Brownlie, J. Colin. Malathion carboxylesterase Patent: US 6235515-A 9 22-MAY-2001;
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Patent: Oakeshort, Galdiam: and Brownitte Malathion carboxylesterase Patent: US 6235515-A 3 22-MAY-2001; Location/Qualifiers 1. 1713 Paramanananananananananananananananananan	Unknown. Unknown. Unknown. Unclassified. Unclassified. 1 (bases 1 to 1713) 1 (bases 1 to 1713) Russell,R.Joyce., Newcomb,R.David., Campbell,P.Malcolm Russell,R.Joyce., Newcomb,R.David., Claudianos,C., Smyth,K		TCGATGTTTGAAAAACATAGAGATTTATTTTAG 1713 	ATTAGTGATGAATTGAAAATGATTGATGTGCCTGAAATGGATAAGATTAAACAATGGAG 1680 	ATGGAAAATGTTTCCTGGGATCCAATTAAGAAATCCGATGAAGTATACAAGTGTTTGAAT 1620 	ACTGGTATATGGATACAATTTGCCACCACTGGTAATCCTTATAGCAATGAAATTGAAGGT 1560 	AATCAATTGGCCAAACGTATGCCTAAAGAATCGCGTGAATACAAAACAATTGAACGTATG 1500 	CGTAGTGGACGTGGTGTAAGGGTGTTAGTCATGCTGATGAATTAACCTATTTCTTCTGG 1440 	GTCTACTTGTATCGCTTCGACTTCGATTCGGAAGATCTTATCAATCCCTATCGTATTATG 1380 	TTCTGGTTCCCCATGCATCGTTTGCTTGCAATTACGTTTCAATCACACCTCCGGTACACCC 1320 	CATGTTACAGGAGAAACACCAACAGCTGATAATTTTATGGATCTTTGCTCTCACATCTAT 1260 	GCTGATGTTGAACGCACCGCCCCAGAGACCTTGGAAATGGGTGCTAAAATTAAAAAGGCT 1200 	CAAATGCCTATGCTTAAAGGAATTGGAAACTTGTGTCAATTTTGTGCCAAGTGAATTG 1140 	ATACCCACTATGATGGGTAACACTTCATATGAGGGTCTATTTTTCACTTCAATTCTTAAG 1080 	

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Russell,R.Joyce., Newcomb,R.David., Campbell,P.Malcoln Robin,G.Charlesde.Quetteville., Claudianos,C., Smyth,Robin,G.Charlesde.Quetteville., Claudianos,C., Smyth,Robin,G.Charlesde.Quetteville., Claudianos,C., Smyth,Robin,G.Charlesde.Quetteville., Claudianos,C., Smyth,Robin,G.Charlesde.Quetteville., Claudianos,C., Smyth,Robin,G.Charlesde.Quetteville., Claudianos,C., Smyth,Robin,G.Charlesde.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Quetteville.Qu
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1 (bases 1 to 2240)

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Newcomb,R.D., Campbell,P.M., Ollis,D.L., Cheah,E., Russell,R..
Oakeshott,J.G.
A single amino acid substitution converts a carboxylesterase to a single amino acid substitution confers insecticide resistance

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97.9%; Score 1676.6; DB 6; Length 1arity 98.0%; Pred. No. 0; Conservative 0; Mismatches 34; Indels:  TCAACGTTAGTTTGATGGAGAAATTAAAATGGAAGATTAAATGCA	SOURCE Unknown.  SOURCE Unknown.  ORGANISM Unclassified.  REFERENCE 1 (bases 1 to 1713)  REFERENCE 1 (bases 1 to 1713)  AUTHORS Russell, R. Joyce., Newcomb, R. David., Robin, G. Charlesde. Quettevi Boyce, T. Mark., Campbell, P. Malcolm., Parker, A. Gerard.,  Oakeshott, J. Graham. and Smyth, KA.  TITLE Enzyme based bioremediation  JOURNAL Patent: US 5843758-A 2 01-DEC-1998;  FEATURES 1. 1713  Source //organism="nuknown"  BASE COUNT 506 a 299 c 363 g 515 t 30 others	OY 1681 TCGATGTTTGAAAACATAGAGATTTATTTTAG 1/13  Db 1978 TCGATGTTTGAAAAACATAGAGATTTATTTTAG 2010  RESULT 8  AR062838  AR062838  LOCUS  DEFINITION Sequence 2 from patent US 5843758.  ACCESSION AR062838.1 GI:5990529  VERSION AR062838.1 GI:5990529	1561 ATGGAAAATGTTTCCTGGGATCCAATTAAGAAAATGTTTCCTGGGATCCAATTAAGAAAATGATTACCTGGGATCCAATTAAGAAAATGATTAAGAAAATGATTAAGAAAATGATTGATGA	Db 1678 CGTAGTGGACGTGGTGTTAAGGGTGTAAGAATGCAATGAACAATTAACCTATTCTCTGG  Oy 1441 AATCAATTGGCCAAACGTATGCCTAAAGAATGCGTGAATAACAATTAAACGTATG  [	Db 1378 CAAATGCCTATGCTTAAGGAATTGGAAACTTGTGTAATTATGTGCCAAGTGAATTG Qy 1141 GCTGATGTTGAACGCACCGCCCCAGAGACCTTGGAAATGGGTGCTAAAATTAAAAAGGCT
1021 A Qy 1021 A Db 1021 A Qy 1081 C O O O O O O O O O O O O O O O O O O	Db Qy 11e., Db Db Qy Db	Qy 661 GCTGCCTTACCCACTACATGATGATGATACTCGCGATAAAACTCGCGGTCTTTGCTGTGGTGAAAGTGCCGGT	1620     Db     481       1917     Qy     541       1680     Db     541       1977     Qy     601	1737	PARAGGET 1437  Qy  61 AAGTTTTTAAACTACCAATGAAACGGTGGTAGCTGAAACTGAATATGGC

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Direct Submission
Submitted (07-MAR-1
ACT 2601, Australia
                                                                                                                         Musca domestica
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Reoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Muscoldea; Muscidae; Musca.

1 (bases 1 to 2100)
Claudianos.c., Russell, R.J. and Oakeshott, J.G.
The same amino acid substitution in orthologous esterases con organophosphate resistance on the house fly and a blowfly Insect Biochem. Mol. Biol. 29 (8), 675-686 (1999)
                                                                                                                                                                                                                                   Musca domestica
AF133341
AF133341.1 GI:
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                                                                                                                        10451921
                                                                                                             (bases 1 to
                                                                          ltted (07-MAR-1999)
2601, Australia
        /dev_stage="4 day
1. .2160
                               /organism="Musca domestica"
/strain="Rutgers Diazinon-R
/db_xref="taxon:7370"
/gene="MdaE7
                         /chromosome="II"
                                                                  Location/Qualifiers
                                                                                                                                                                                                                                    GI:4768932
                                                                                                    Russell, R.J.
                                                                                                              2160)
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                                                                                   Entomology,
                third
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                                                                                                    Oakeshott, J.G.
                instar larvae"
                                                                                   CSIRO, Clunies
                                        (R+)"
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                                                                                   Ross,
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                                                                                   Canberra,
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AATGTGCCCGGTAATGCCGGCCTTAAAGATCAAGTCATGGCCTTGCGTTGGATTAAAAAT
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VTVQXRLGVLGFLSLKSENLNVPGNAGLKDQVMALRWVKSNIANFGGDVDNITVFGES
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DILEFLMKANPYDLIKBEPQVLIPEEMONKVNFPFGFPVFPYQTADCVVPKPIREMVK
SAWGNSIPTLIGNTSYEGLLFKSIAKQYPEVKELESCVNYVPWELADSERSAPETLE
RAAIVKKANPOGETPTLDNFMELCSYFYTLFPMHRFLQLFRHTMGTPIYLYRFDPDS
EEIINPYRINREGROVGGVSHADELTVLFWNILSKRLFKESREYKTIERMVGIWTEFA
TTGKPYSNDIAGMENLTWDPIKKSDDVYKCLNIGDELKVMDLPENDKIKQWASIFDKK
KELF"
2115: 2120
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                                               ATTAGTGATGAATTGAAAATGATTGATGTGCCTGAAATGGATAAGATTAAACAATGGGAG
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JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE
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                AAAGTGAAAGGCGTTAAACGTTTAACTGTGTACGATGATTCCTACTACAGTTTTGAGGGT
                                                              AAAATTTTAAACTACCGCCTTATTACCAATGAAACGCATATTGTCGATACGGAATATGGA
                                                                              AAGTTTTTAAACTATCGTTTAACTACCAATGAAACGGTGGTAGCTGAAACTGAATATGGC
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Guerrero, F.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haematobia irritans irritans
Eukaryota; Metazoa; Arthropoda; He
Neoptera; Endopterygota; Diptera;
Muscoldea; Muscidae; Haematobia.
1 (bases 1 to 2175)
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TAWGNSIPTLIGNTSYEGLLFISVGKQNPHLIKELETFECYVPGELVVEDRSSPESLE
IASILKKLYVRGETPTLESFTELCSDFYFWYPMHRFLQLRFNHTVGSPIYLYRFDFDS
                                                                                                                                                                                                                                                                                                                                                                                       /translation="MNENVSFLEKLRWKIKCVENKILNYRLITNETHIVDTEYGKIKG
VKRLTYVDDSFYSFEGIDYAKPPVGELERKAPQRPPYPDGVKDCHAASRSVQTDFIS
GNSSGSEDCLXLNVYTNHLNYDTKRPVLVFFHGGFICGEANRNYYGADYFIKKDVPI
ITVQYELGVLGFLSLNSENLNVPGNAGLKDQVVAALRWIKNNCASFGGDPDCITLFGES
AGAASTHYMMITEQARGLFHRAVLMSGTAMCIWAHTQCQHRGYTIAKRIGYKGENNDK
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TTGNPYSPEINGMENTTWDSLKKSDEVYKCMNIGDELKFIDLPEMEKLKVWQSVFNKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="alpha E7 esterase"
/protein_id="AAF14517.1"
/db_xref="GI:6502939"
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282. .1994
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/sub_species="irritans"
/db_xref="taxon:75445"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar
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                                             ACTACAGTTTTGAGGGTATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAAG
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Russell,R.Joyce, Newcomb,R.David., Campbell,P.Malcolm.,
Robin,G.Charlesde.Quetteville., Claudianos,C., Smyth,K.-A.,
Boyce,T.Mark., Oakeshott,J.Graham. and Brownlie,J.Colin.
Malathion carboxylesterase
Malathion carboxylesterase
Patent: US 6235515-A 14 22 MAY-2001;
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/organism="Drosophila
/strain="y; cn bw sp"
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Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J.,
Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J.,
Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R.,
Gonzalez, M., Guarin, H., Li, P., Liao, G., Miranda, A., Mungall, C. J.,
Gonzalez, M., Guarin, H., Li, P., Liao, G., Miranda, A., Mungall, C. J.,
Runnoo, J., Pacleb, J., Paragas, V., Park, S., Phouanenavong, S., Wan, K.
Yu, C., Lewis, S. E., Rubin, G.M. and Celniker, S.
Direct Submission
Direct Submission
                                                                                                                                           sequence clones from Drosophila Gene Collection I (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular cDNA clone. However, there are artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAs, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanoĝaster

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 2017)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (10-AUG-2001) Berkeley Drosophila Genome Lawrence Berkeley National Laboratory, One Cyclotro Berkeley, CA 94720, USA Sequence submitted by:
                                             reverse transcriptase errors that result in single base changes. For further information about this sequence, including its location and relationship to other sequences, please visit our Web site (http://fruitfly.berkeley.edu) or send email to
                                                                                                                                                                                                                                                                                                                                                                                                                                      Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
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cdna@fruitfly.berkeley.edu.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                              Berkeley, CA 94720
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           AATTGCGCCAACTTTGGTGGCAATCCCGATAATATTACAGTCTTTGGTGAAAGTGCCGGT
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nilarity 62.6%;
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/gene="alpha-Est7"
/note="alignment with genomic scaffold AE003671"
/db_xref="FLYBASE:FBgn0015575"
91..1809
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Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
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Neoptera; Endopterygota; Diptera; Brachycera;
Pephydroidea; Drosophilidae; Drosophila.
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Location/Qualifiers
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DSKHFNIMRIITCGRKVRGTCHADDLSYLFYNAAAKKLKRRTAEFKTIKRLVSMVVHF
                                                                                                                                                      AGGASTHYMMLTDQAKGLFHKTIIMSGSALAPWAQTPTHINWPYRLAQATGYTGDAND
RDIFAHLKKCRASSMLKVAEDIITMEERHQRLTMFSFGPTIEPYLTPHCVIPKSPLEM
MRDCWGNSIPMVIGGNSFEGLLMFPEVNKWPELLCQLGDCENLAPQDAHVDEQQRKAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"Longest ORF"
/codon_start=1
                                                                            AISGDPNIPMVCQDEKEQPRGAWLPISKDDKVFQCLNISHDVHVIDLPEAEKLRLWDC
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                                                                                                                                                                            ACCATGTTCAGCTTTGGACCCACCATCGAGCCCTATTTGACTCCTCATTGTGATTCCC
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                                  GGAAACTCCTTCGAAGGTCTCCTCATGTTTCCCGAAGTGAACAAGTGGCCGGAACTGCTT
                                                                   AACACTTCATATGAGGGTCTATTTTTCACTTCAATTCTTAAGCAAATGCCTATGCTTGTT
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Pred. No. 2.5e-
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                                                                                                                                l (bases 1 to 2820)

Robin,C., Medveczky,K.M., Russell,R.J. and Duplication and Divergence of the genes of cluster of Drosophila melanogaster

J. Mol. Evol. (1996) In press
(bases 1 to 2820)
                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                  Submitted (11-MAR-1996) Charles Robin, Biotechnology, CSIRO Entomology, Clunies Ross Street, Canberra, ACT 2601, Austral
                                                                                                                                                                                                                                                                                            Drosophila melanogaster
U51050
U51050.1 GI:1272313
                                                                                                                 Direct Submission
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Drosophila melanogaster
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                                    /organism="Drosophila
/db_xref="taxon:7227"
                                                                        y, Clunies Ross Street,
Location/Qualifiers
             /map="84D3"
 note-"Yac
clone DY219"
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the alpha-esterase
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Query Match
Best Local Sin
Matches 1054;
563 TTAAAGATCAAGTCATGGCCTTGCGTTGGATTAAAAATAATTGCGCCAACTTTGGTGGCA
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                                                                                                                                      TGGTGCTTTGGGTAATCTACTGTGTGCGTATGCGCAATATTTTGACTAAACATTATTGTA 1489
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                                                           CCTACACAGGATTTATGAGTCTTAAGTCCCCCGAGCTAAATGTACCAGGAAATGCTGGCC
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/protein_id="AAB01149.1"
/db_xref="GI:1272314"
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/EC_number="3.1.1"
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Pred. No. 2.9e-72;
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  CTGCCACGGGTAATCCCTACAGCGAGAAGATCAACGGTATGGACACTCTGACCATTGATC
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                                                                                                    CTAAAGAATCGCGTGAATACAAAACAATTGAACGTATGACTGGTATATGGATACAATTTG
                                                                                                                                                                                  GTGTTAGTCATGCATGATGAATTAACCTATTTCTTCTGGAATCAATTGGCCAAACGTATGC
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                                                                           CGAAGGAAAGTCGCGAGTACAGGAACATCGAACGAACCGTGGGCATCTGGACCCAGTTTG
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GTGTACACCAACAATGTGAGTAATTCTATTAACTTGTGTACATAAAACATCGTTAAAAACC
                              GTCTATACGAATAAT---
                                                              CCCCAGCGACCAACACCCTGGGATGGTGTGCGTGATTGTTGCAATCATAAAGATAAGTAA
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AC015272
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* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is avai

* the accession number will be preserved.

Location/Qualifiers
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Drosophila melanogaster
Drosophila melanogaster
Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 5735)
1 (bases 1 to 5735)
Adams, M. and Venter, J.C.
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to fly@celera.com
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1383	THE OTHER OCCUPATION OF THE ACTION OF THE OTHER PROPERTY.	1243	ž
35042	AAGCACCCCAGATAATTACATGGATGTAAGTGTCGTCCAATTAGGTGCTTACATAATCAT	35101	Ъ
1242	CCAACAGCTGATAATTTTATGC	1218	ν
35102	   AAAGAAAAACTGGATTCGTGG	16	β ;
2 5 15	AATTTUTECCAAGGAATTGCTGATGTTGAAC 	35221	5 8 2
52	TCTTTCAATAAGTAAATTTAATTTTAATTTTAACAATTCTTAAGCAAATGCCTATGCTT	2 2 0	5 B 5
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682 35702	ATCCCGATAATATTACAGTCTTTGGTGAAAGTGCCGGTGCTGCCTCTACCCACTACATGA	623 35761	유 성
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Search completed: April 11, 2003, 06:01:19 Job time: 3017.03 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Result	Score	Query Match	Query Match Length DB ID	DB	ID	Description
_	1701.8	99.3	1713	16	AAQ91561	OP-sensitive ester
2	1701.8	99.3	1713	18	AAT68596	Lc-alpha-E7 malath
w	1681	98.1	1713	16	AAQ91566	OP-resistant ester
4	1677.8	97.9	1713	16	AAQ91564	OP-resistant ester
ъ	1677.8	97.9	1713	16	AAQ91565	OP-resistant ester
6	1676.2	97.9	1713	16	AAQ91563	OP-resistant ester
7	1674.6	97.8	1713	16	AAQ91562	OP-resistant ester
8	956.6	55.8	1710	18	AAT68597	Md-alpha-E7 gene.
9	677.2	39.5	2001	23	ABL02067	Drosophila melanog

PI PI

Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG; Parker AG, Robin GC, Russell RJ, Smyth K;

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ABLC11/4 ABLC1942 ABLC2029 ABLC1946 ABLC1946 AAV40767 AAV407743 AAD21169	AAV40756 AAV40757 AAV40754 AAV40755	ABL19064 ABL01945 ABL01858 AAV40764 AAV40765	ABL02102 ABL02102 ABL02080 ABL02098 ABL02100 AAV40762 AAV40763	ABL02066 ABL02099 ABL04689 ABL02103 ABL01859 ABL02101 ABL02101 ABL02101 ABL02101 ABL0247 ABL0332 ABL07668 ABA90480 ABA90480 ABA90480	ABL02081
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## ALIGNMENTS

RESU AAQ9 ID XX AC	RESULT 1 AAQ91561 ID AAQ91561 standard; cDNA; 1713 BP. XX AC AAQ91561;
XX	22-DEC-1995 (first entry)
XX	OP-sensitive esterase E3 Lc743 clone.
X	Esterase; E3; bioremediation; organophosphate; carbamate;
KW	
ΥX	SS.
SO	Lucilia cuprina.
×	
FH	Key Location/Qualifiers
FΤ	CDS 11713
FΤ	/*tag= a
×	
PN	WO9519440-A1.
X	
PD	20-JUL-1995.
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ΡF	13-JAN-1995; 95WO-AU00016.
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PR	13-JAN-1994; 94AU-0003347.
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Best Local Sim
Matches 1706;
                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA from organophosphate (OP)-sensitive L. cuprina pupa cDNA Library was amplified using cluster-specific esterase primers Isolated clone Lc743, a probable full-length cDNA, was expressed using a baculovirus vector in insect cells and shown to encode an OP-susceptible E3 esterase, useful in bioremediation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pure E3 esterase from eliminate residues of water, meat etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1995-263870/34.
P-PSDB; AAR78142.
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                                                      AATTGCGCCAACTTTGGTGGCAATCCCGATAATATTACAGTCTTTGGTGAAAGTGCCGGT
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RESULT 2
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ID AAT6
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standard;

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AAT68596;

08-AUG-1997

(first

entry)

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                                                                                              ACTGGTATATGGATACAATTTGCCACCACTGGTAATCCTTATAGCAATGAAATTGAAGGT
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Query Match
Best Local Similarity
                                                             DNA molecule Lc743 (AAT68596) codes for an esterase (AAW17765) fr a malathion susceptible strain of Lucilia cuprina. Comparison with a consensus sequence from derived from clones of the Lc-alpha-E7 resistant allele (see also AAW17768) indicated only creplacement site difference, a Trp to Leu substitution at amino acid position 251 (nucleotide position 752). This mutation is an excellent candidate for the malathion resistance mutation. The resistant enzyme acts as a malathion carboxylesterase and can be formulated for use in degrading environmental carboxylester, or dimethyl general organophosphates.
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                                        Sequence 1713
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DB; AAW17765.
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Oakeshott
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remediation; bioremediation; deco
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                 RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding OP-susceptible esterase E3 of L. cuprina) from a diazinon resistant strain, Llandillo 103. 4 Isolated clones were sequenced (Lc7L103 A-D, AAQ91562-65) that encoded diazinin-resistant esterases. The esterases, or cells expressing them, are used in bioremediation.
                                                                                                                Pure E3 esterase from eliminate residues of
                                                                                    Example 4; Page 12-17;
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insecticide; |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGTAGTGGACGTGGTGTTAAGGGTGTTAGTCATGCTGATGAATTAACCTATTTCTTCTGG
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                                                                                                                                                            cuprina
                                                                                                                                                                                                       bioremediation;
pesticide; water
                                                                                                                                                                                                                                                 esterase Lc7L103B
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                  95WO-AU00016
                                                                                                  Location/Qualifiers
1..1713
/*tag= a
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                                                                                                                                                                                                        organophosphate;
decontamination;
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decontamination;

13-JAN-1994;

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Best Local Sim
Matches 1690;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Boyce 1
Parker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 4; Page 12-17; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                water, meat etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           eliminate
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                      601
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                  AATTGCGCCAACTTTGGTGGCAATCCCGATAATATTACAGTCTTTGGTGAAAGTGCCGGT
                                                           ATTAACATACAATATCGTTTGGGAGCTCTAGGTTTTCTAAGTTTAAATTCAGAAGACCTT
                                                                                                                                           GGTGAAAATCATCGTGATATGTATGGTCCTGATTATTTCATTAAAAAGGATGTGGTGTTTG
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                                                                                                                                                                                                                                                                                                            AAAGTGAAAGGCGTTAAACGTTTAACTGTGTACGATGATTCCTACTACAGTTTTGAGGGT
                                                                                                                                                                                                                                                                                                                                                                                                      AAGTTTTTAAACTATCGTTTAACTACCAATGAAACGGTGGTAGCTGAAACTGAATATGGC
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te residues of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.9%;
98.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lucilia cuprina and related DNA organo:phosphate and carbamate p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1676.2;
Pred. No. 0;
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J, Smyth K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 16; Length
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pesticides
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	TCGATGTTTGAAAAACATAGAGATTTATTTTAG 1713	1681 1681	Qy Db
1680	ATTAGTGATGAATTGAAAATGATTGATCTGCCTGAAATGGATAAGATTAAACAATGGGAG	1621	Qу
1680		1621	Дъ
1620	ATGGAAAATGTTTCCTGGGATCCAATTAAGAAATCCGATGAAGTATACAAGTGTTTGAAT	1561	.pb
1620		1561	
1560	ACTGGTATATGGATACAATTTGCCACCACTGGTAATCCTTATAGCAATGAAATTGAAGGT	1501	Db .
1560		1501	
1500 1500	AATCAATTGGCCAAACGTATGCCTAAAGAATCGCGTGAATACAAAACAATTGAACGTATG	1441 1441	Оу
1440	CGTAGTGGACGTGGTGTTAAGGGTGTTAGTCATGCTGATGAATTAACCTATTTCTTCTGG	1381	Qy
1440		1381	Db
1380 1380	GTCTACTTGTATCGCTTCGACTTCGATTCGGAAGATCTTATCAATCCCTATCGTATTATG	1321 1321	Qу
1320	TTCTGGTTCCCCATGCATCGTTGCTTGCAATTACGTTTCAATCACACCTCCGGTACACCCC	1261	Qy
1320		1261	Db
1260	CATGTTACAGGAGAAACACCAACAGCTGATAATTTTATGGATCTTTGCTCTCACATCTAT	1201	
1260		1201	Db
1200	GCTGATGTTGAACGCACCGCCCCAGAGACCTTGGAAATGGGTGCTAAAATTAAAAAGGCT	1141	Qy
1200		1141	Db
1140	CAAATGCCTATGCTTGAAGGAATTGGAAACTTGTGTCCAATTTTGTGCCAAGTGAATTG	1081	Qy
1140		1081	Db
1080	ATACCCACTATGATGGTAACACTTCATATGAGGGTCTATTTTTCACTTCAATTCTTAAG	1021 1021	Оy
1020	GCTGATTGTGTCTTACCCAAACATCCTCGGGAAATGGTTAAAACTGCTTGGGGTAATTCG	961	Qy
1020		961	Db
960	GAAGAGCGTACAAATAAGGTCATGTTTCCTTTTGGTCCCACTGTTGAGCCATATCAGACC	901 901	Ор
900	TTTCTTATGAAAGCCAAGGCACAGGATTTAATAAACTTGAGGAAAAAGTTTTAACTCTA	841	Qу
		841	ДЬ
840 840	TTCACCTTAGCCAAATTGGCCGGCTATAAGGGTGAGGATAATGATAAGGATGTTTTGGAA	781 781	Фр
780	ATACTAATGTCGGGTAATGCTATTTGTCCATTGGCTAATACCCAATGTCAACATCGTGCC	721	Qy
780		721	Db
720		661	Db .

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Best Local Sim
Matches 1689;
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                                                                                                                                                                                                                                                                                                                                                                                                                        13-JAN-1994;
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                                                    ATACCGTACGCCCAACCGCCAGTGGGTGAGCTTGAGATTTAAAGCACCCCAGCGACCAACA
                                                                                        AAAGTGAAAGGCGTTAAACGTTTAACTGTGTACGATGATTCCTACTACAGTTTTGAGGGT
                                             ATACCGTACGCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCACCCCAGCGACCAACA
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Robin GC
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                                                                                                                                                                                       Conservative
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98.6%;
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Pred. No. 0;
0; Mismatches
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Smyth K;
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No. 0;
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d carbamate pesticides
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                                                                                                                       GAAGAGCGTACAAATAAGGTCATGTTTCCTTTTGGTCCCACTGTTGAGCCATATCAGACC
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CGTAGTGGACGTGGTTAAGGGTGTTAGTCATGCTGATGAATTAACCTATTTCTTCTGG
                                                                                                                                                           CAAATGCCTATGCTTGAAGGAATTGGAAACTTGTGTCAATTTTGTGCCAAGTGAATTG
                                                                                                                                                                                                      ATACCCACTATGATGGGTAACACTTCATATGAGGGTCTATTTTTCACTTCAATTCTTAAG
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                  GTCTACTTGTATCGCTTCGACTTCGATTCGGAAGATCTTATTAATCCCTATCGTATTATG
                                                                                                                                                                                              ATACCCACTATGATGGGTAACACTTCATATGAGGGTCTATTTTTCACTTCGTTTCTTAAG
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RESULT 8
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A 1710 bp DNA molecule (AAT68597) comprises the Md-alpha-E7 coding sequence of the Musca domestica Rutgers strain. It was isolated by amplification of genomic DNA using alpha-esterase consensus primers (see also AAT68598-99) and use of a 534 bp amplicon to screen a genomic library of M. domestica. A mutation of the gene, resulting in substn. of serine for tryptophan at amino acid position 251 (see also AAW17767), confers malathion
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                                                                                                                                                                                                                   encoding enzyme that degrades organophosphate pesticides ful for decontamination of soil, water, food etc
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DB; AAW17767.
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D, Oakeshott JG, Robin GC,
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Best Local Sim
Matches 1223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             resistance. The resistant enzyme acts as a malathion carboxylesterase and can be formulated for use in degrading environmental carboxylester or dimethyl general organophosphates
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               TTGAGCCATATCAGACCGCTGATTGTGTCTTACCCAAACATCCTCGGGAAATGGTTAAAA
                                                                                                                                                                             AATGTCAACATCGTGCCTTCACCTTAGCCAAATTGGCCGGCTATAAGGGTGAGGATAATG
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73.4%;
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No. 8.8e-253;
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23-MAR-2000;
11-JUL-2000;
                              23-MAR-2001;
                                                  27-SEP-2001
                                                                     WO200171042-A2
                                                                                          Drosophila melanogaster
                                                                                                              Drosophila; developmental biology;
pharmaceutical; gene; ss.
                                                                                                                                           Drosophila
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                                                                                                                                                                                   ABL02067;
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                                                                                                                                           melanogaster expressed polynucleotide
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2000US-0614150
                              2001WO-US09231
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Query Match
Best Local :
                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventiuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                            The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wlpo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                        Claim 1;
                                                    Sequence
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                AATGTGCCCGGTAATGCCGGCCTTAAAGATCAAGTCATGGCCTTGCGTTGGATTAAAAAT
                                                                                                                                  GGTGAAAATCATCGTGATATGTATGGTCCTGATTATTTCATTAAAAAGGATGTGGTGTTG
                                                         GTCACGATACAGTACCGACTTGGGGCTTTGGGATTTATGAGTCTTAAGTCCCCCGAGCTA
                                                                      ATTAACATACAATATCGTTTTGGGAGCTCTAGGTTTTCTAAGTTTAAATTCAGAAGACCTT
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                                                                                    AATATTAGTGATGAATTGAAAATGATTGATGTGCCTGAAATGGATAAGATTAAACAATGG
                                                                                                                                   GGTATGGACACTCTGACCATTGATCCAGTTCGCAAATCCGACGAGGTCATCAAGTGCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01810-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB07373-ABB72072).
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABLIG511), expressed DNA sequences (ABLIG176-ABLIG511), expressed DNA sequences (ABLIG176-ABLIG511).

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The sequence data for this patent did not form specification, but was obtained in electronic at ftp.wipo.int/pub/published\_pct\_sequences.

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CACAGGATTTAATAAAACTTGAGGAAAAAGTTTTAACTCTAGAAGAAGAGGGTACAAATAAGG 919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent
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genes from Drosophila and
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11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1665 BP; 397 A; 446 C; 468 G; 354 T; 0 other;
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P-PSDB; ABB57996.
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Local Similarity 52.4%;
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CAAAGAATTTGTATCCCACCAAACCAATGCCCGTGATGGTCTGGATCTATGGCGGTGGCT
                CCCCGGAGGTCTGGACGGAGGTCAGGAGCTGCACCTCCCAGGGTCCCAAGCCACTGCAGA 244
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                                                                                         TTGATTTTATAACGGGCAAAGTGTGTGGCTCAGAGGATTGTCTATACCTAAGTGTCTATA 352
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Pred. No. 6.7e-91;
0; Mismatches 773; Indels '9; Gaps
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487 CAATTGAACGTATGACTGGTATATGGATACAATTTGCCACCACTGGTAATCCTTATAGCA	1427 CCTATTTCTTCTGGAATCAATTGGCCAAACGTATGCCTAAAGAATCGCGTGAATACAAAA 1486	1367 CCTATCGTATTATGCGTAGTGGACGTGGTGGTTAAGGGTGTTAGTCATGCTGATGAATTAA 1426	1307 CCTCCGGTACACCCGTCTACTTGTATCGCTTCGACTTCGATTCGGAAGATCTTATCAATC 1366	1247 GCTCTCACATCTATTTCTGGTTCCCCATGCATCGTTTGTTGCAATTACGTTTCAATCACA 1306	1187 AAATTAAAAAGGCTCATGTTACAGGAGAAACACCAACAGCTGATAATTTTATGGATCTTT 1246	1133 GTGAATTGGCTGATCTTGAACGCACCGCCCCAGAGACCTTGGAAATGGGTGCTA 1186	1073 TTCTTAAGCAAATGCCTATGCTTGTTAAGGAATTGGAAACTTGTGTCAATTTTGTGCCAA 1132	1013 GTAATTCGATACCCACTATGATGGGTAACACTTCATATGAGGGTCTATTTTTCACTTCAA 1072	953 ATCAGACCGCTGATTGTGTCTTACCCAAACATCCTCGGGAAATGGTTAAAACTGCTTGGG 1012 	893 TAACTCTAGAAGAGCGTACAAATAAGGTCATGTTTCCTTTTGGTCCCACTGTTGAGCCAT 952	833 TTTTGGAATTTCTTATGAAAGCCAAGGCACAGGATTTAATAAAACTTGAGGAAAAAGTTT 892 	773 ATCGTGCCTTCACCTTAGCCAAATTGGCCGGCTATAAGGGTGAGGATAATGATAAGGATG 832	713 ATCGTGGTATACTAATGTCGGGTAATGCTATTTGTCCATTGGCTAATACCCAATGTCAAC 772	653 GTGCCGGTGCTGCCTCTACCCACTACATGATGTTAACCGAACAAACTCGCGGTCTTTTCC 712	593 TTAAAAATAATTGCGCCAACTTTGGTGGCAATCCCGATAATATTACAGTCTTTGGTGAAA 652 	533 AAGACCTTAATGTGCCCGGTAATGCCGGCCTTAAAGATCAAGTCATGGCCTTGCGFTGGA 592 	473 TGGTGTTGATTAACATACAATATCGTTTGGGAGCTCTAGGTTTTCTAAGTTTAAATTCAG 532	413 TTATTATCGGTGAAAATCATCGTGATATGTATGGTCCTGATTATTTCATTAAAAAGGATG 472

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pharmaceutical; gene; ss.
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                                                                                                  The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
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Pred. No. 4.1e-90;
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The invention relates to an isolated nuccapable of detecting 1000 or more genes
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                                                                                                                      TGTTTTGGAATTTCTTATGAAAGCCAAGCCACAGGATTTAATAAAACTTGAGGAAAAAGT
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                                                                                    Drosophila melanogaster
                                                                                                             pharmaceutical;
                                                                                                                         Drosophila;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
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11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
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genes from Drosophila
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DB; ABB57756.
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TTGGATGTGCCCGGAAATGCTGGTCTCAAGGACCAAGTGATGGCCCTTCGCTGGATCAGT
                                                                         TTGATTAACATACAATATCGTTTGGGAGCTCTAGGTTTTCTAAGTTTAAATTCAGAAGAC
                                                                                                                                 ATCGGTGAAAATCATCGTGATATGTATGGTCCTGATTATTTCATTAAAAAGGATGTGGTG
                                                                                                                                                                                            AAGATCGTCCAGTATCGCCTTGGCACAAAGCAGACGAAGGTGGTCTGCACCAGGGATGGC
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A1388926 GH19977.5
A1403369 GH23036.5
A1517692 GH28740.5
B1609541 RH14337.5
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1631806 RH61455.	1572606 RH08182.	30054 RH59016	1622392 RH54254.	1607309 RH74350.	I567399 RH37771.	I624437 RH63994.	1638519 SD20822.	517539 GH28541.5	I588504 RH29849	1617897 RH48369.	389766 GH21022.5	1370683 RE57396	134524 GH12012.	.1134360 GH11805.	107729 GH05557.5	1575862 RH32195	G641228 SD12519.	513346 GH26524.5	I564361 RH37254	516869 GH27454.	403830 GH23353.	109573 GH08808.5	I621302 RH52624	1588370 RH29561.	1614821 RH44296.	1619037 RH49995.	BI564586 RH61888.	П108156 GH06911.	108080 GH06811.	I293416 LP06524.	109901 GH09292.	403098 GH22464.	113763 GH10213.5	I233202 RE29491.	1614443 RH43812.	BI614181 RH43493.5	1639486 SD22067.	1635372 SD16705.

## ALIGNMENTS

TITLE JOURNAL COMMENT ACCESSION VERSION KEYWORDS SOURCE RESULT 1
AI062034
LOCUS
DEFINITION FEATURES REFERENCE AUTHORS ORGANISM Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 778)

1 (bases 1 to 778)

1 (bases 1 to 778) Lawrence Berkeley National Lab One Cyclotron Rd, Berkeley, CA 94720, USA Fax: 510 486 6798 Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu Plate: 10 row: G column: 4 AIO62034 778 bp mRNA linear EST 19-APR-GH01076.5prime GH Drosophila melanogaster haad pOT2 Drosophila melanogaster cDNA clone GH01076 Sprime similar to U51050: Drosophila melanogaster alpha esterase (aE7) gene, partial cds, High quality sequence stop: 363
Location/Qualifiers BDGP Contact: Stapleton, M. Harvey, D., Brokstein, P., Hong, L., Lewis, S. and Rubin, G.M. BDGP/HHMI Drosophila EST Project Unpublished (2001) EST AI062034.1 GI:3337873 mRNA sequence. AI062034 fruit fly. Evans-Holm, M., Su, C., Tsang, G., EST 19-APR-2001

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RESULT 2
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AI388926 649 bp mRNA linear EST 19-APR GH19977.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH19977 5prime similar to US1050: Drosophila melanogaster alpha esterase (aE7) gene, partial cds
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//Ob_xref="taxon:7227"
//Ob_xref="taxon:7227"
//Clone="GHO1076"
//Clone_lib="GH Drosophila melanogaster head pOT2"
//Clone_lib="GH Drosophila melanogaster head pOT2"
//Cex="male and female"
//Cex_stage="adult"
//Lab_host="DH5 - alpha"
//Lab_host="DH5 - alpha"
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431 ATCGTGATATGTATGGTCCTGATTATTTCATTAAAAAGGATGTGGTGTTGATTAACATAC 490
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                          TGAAAGCCAAGCCACAGGATTTAATAAAACTTGAGGAAAAAGTTTTTAACTCTAGAAGAGC
                                                                                                            TAGCCAAATTGGCCGGCTATAAGGGTGAGGATAATGATAAGGATGTTTTGGAATTTCTTA 847
                                                                                                                                                                                                                                                                                                     CCCACTACATGATGTTAACCGAACAAACTCGCGGTCTTTTCCATCGTGGTATACTAATGT 730
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AGAACGTAAAGGCCAAGGATCTTATTCGCGTGGAGGAAAATGTCCTGACACTGGAGGAAC
                                                                                         TAGCCAAGCTGGTTGGCTACAAGGGCGAGGACAACGACAAGGATGTGCTGGAGTTCTTGC
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AI388926.1 GI
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Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST
Unpublished (2001)
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Plate: 199 row: G
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
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quality sequence stop:
Location/Qualifiers
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/clone=lib="GH Drosophila melanogaster head pOT2."
/sex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
/note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2: XhOI; Sized fractionated cDNAs were directly ligated into pOT2. Plasmid cDNA library."
a 160 c 172 g 152 t
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/db_xref="taxon:7227"
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Berkeley, CA
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 ATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCACCCCAGCGACCAACA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plate: 230 row: C column: 12 High quality sequence stop: 648
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1 (bases 1 to 688)
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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One Cyclotron Rd, Berkeley, CA
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/note="Organ: head; Vector: pOT2; Site_1: EcoRi; Site
/note="Organ: head; Vector: pOT2; Site_1: EcoRi; Site
Xhoi; Sized fractionated cDNAs were directly ligated
pOT2. Plasmid cDNA library."
174 c 197 g 156 t
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/sex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
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/db_xref="taxon:7227"
/clone="GH23036"
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Pred. No. 3.5e-61;
0; Mismatches 208;
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                                                                                                                                                                                                                                                                       Length 688;
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                                                                                                                                                                                                                                                                                                                                                                                 Email: http://www.fruitfly.org/EST, Plate: 287 row: D column: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BDGP/HHMI Drosophila EST Project Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Harvey,D., Brokstein,P., Hong,L., Lewis,S. and Rubin,G.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                                                                            One Cyclotron Rd, Berkeley, CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Stapleton, M.
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                                                                            /clone_lib="GH Drosophila melanogaster hea
/sex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
/note="Organ: head; Vector: pOT2; Site_1:
xho1; Sized fractionated cDNAs were direct
xho1; Sized fractionated cDNAs vere direct
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                                                                                                                                                                     Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Misra, S., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and Rubin
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Step by mrNA linear EST 07-SEP-2001 RH14337.5prime RH Drosophila melanogaster normalized Head pFlc-1 prosophila melanogaster cDNA clone RH14337 5 similar to alpha-Est7: FBan0001112 GO:[carboxyesterase (GO:0004091); carboxyesterase (GO:0004091)] located on: 3R 84D5-84D5;: 08/17/2001, mRNA sequence
                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygoneoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                      Lawrence Berkeley One Cyclotron Rd, Fax: 510 486 6798
                                                                                                                                                      Phouanenavong,S.,,G.M.
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Drosophila melanogaster
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         est@fruitfly.berkeley
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTGGCTCAGAGGATTGTCTATACCTAAGTGTCTATACGAATAATCTAAATCCCGAAACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCGACTGCAGCCAGCCGAAGGATAAGGCCGTCCAGGTGCAGTTCGTCTTCGATAAGGTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCCAGTCGACCAATGAAACAGTTGTCGCCGACACGGACACGGGCCAAGTGAGGGGTATCA 120
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                                                                                                                                                                                                                    CTGGCCTCAAGGATCAGGTGCTGGCCCT
                                                                                                                                                                                                                                                        CCGGCCTTAAAGATCAAGTCATGGCCTT 584
                                                                                                                                                                                                                                                                                      GACTTGGGGCTTTGGGATTTATGAGTCTTAAGTCCCCCGAGCTAAATGTACCAGGAAATG
                                                                                                                                                                                                                                                                                                          GTTTGGGAGCTCTAGGTTTTCTAAGTTTAAATTCAGAAGACCTTAATGTGCCCGGTAATG
                                                                                                                                                                                                                                                                                                                                                             AATGGTATGGCCCGGATTACTTTATGAAAGAAGATGTTGTTCTCGTCACGATACAGTACC
                                                                                                                                                                                                                                                                                                                                                                                  ATATGTATGGTCCTGATTATTCATTAAAAAGGATGTGGTGGTTGATTAACAATATC
                                                                                                                                                                                                                                                                                                                                                                                                                                    CTCGCCCGGTTATGGTTTGGATTCACGGAGGAGGCTTCATTATCGGCGAGGCCAATCGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGGCTCCGAGGACTGCCTCTATCTCAATGTGTACACCAACAATGTGAAGCCCGACAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTCCGGTGGGGGAGTTGCGGTTTAAGGCCCCTCAGAGGCCCATTCCCTGGGAGCGAGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 447.
Location/Qualifiers
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                                             B1628316

B1628316

B1628316

RH56682.5prime RH Drosophlia melanogaster ormalized Head pFlc-1

Drosophila melanogaster cDNA clone RH56682 5 similar to alpha-Est7:

FBan0001112 GO: [carboxyesterase (GO:0004091); carboxyesterase (GO:0004091)] located on: 3R 84D5-84D5; 08/22/2001, mRNA sequence.
                                 BI628316
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/dev_stage="Adult"
/lab_host="DH5-alpha TonA"
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/db_xref="taxon:7227"
/clone="RH14337"
/clone_lib="RH Drosophila
                GI:15530524
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Pred. No. 2.9e
0; Mismatches
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KEYWORDS
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ORGANISM
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                     CAAGTGAGGGGTATCAAGCGTCTATCTCTCTACGATGTGCCCTACTTCAGCTTCGAGGGT
                                                                  GGTGAAAATCATCGTGATATGTATGGTCCTGATTATTTCATTAAAAAAGGATGTGGTGTTG
                                        GTGAAGCCCGACAAGGCTCGCCCGGTTATGGTTTGGATTCACGGAGGAGGCTTCATTATC
                                                                                                                                               ATAACGGCAAAGTGTGTGGCTCAGAGGGATTGTCTATACCTAAGTGTCTATACGAATAAT 360
                                                                                                                                                                                                                                             CCCTGGGATGGTGTGCGATTGTTGCAATCATAAAGATAAGTCAGTGCAAGTTGATTTT 300
                                                                                                                                                                                                                                                                                                                                                                                              AAAGTGAAAGGCGTTAAACGTTTAACTGTGTACGATGATTCCTACTACAGTTTTGAGGGT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAGTCCAGCAGTATCGCCAGTCGACCAATGAAACAGTTGTCGCCGACACGGAGTACGGC
                                                                                                                         GTCTTCGATAAGGTAGAGGCTCCGAGGACTGCCTCTATCTCAATGTGTACACCAACAAT 470
                                                                                                                                                                                                                                                                                          ATCCCGTACGCCCAGCCTCCGGTGGGGGAGTTGCCGGTTTAAGGCCCCTCAGAGGCCCATT
                                                                                                                                                                                                                                                                                                               ATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCACGCCAGCGACCAACA
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                                                                                                                                                                                                    CCCTGGGAGCGAGTTCGCGACTGCAGCCAGCCGAAGGATAAGGCCGTCCAGGTGCAGTTC 410
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367; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Muscc
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 674)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: http://www.fruitfly.org/EST, Plate: RH.566 row: G column: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., Georg, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Misra, S., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Physial Revision of Company of Chamber, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and Rubi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                One Cyclotron Rd, Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BDGP/HHMI RH Drosophila EST Project Unpublished (2001)
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Location/Qualifiers
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/lab_host="DH5-alpha TonA"
/lab_host="DH5-alpha TonA"
/note="Organ: head; Vector: pFlc1; Site_1: XhoI; Site_2:
/note="Organ: head; Vector: pFlc1; Site_1: XhoI; Site_2:
/note="Organ: head; Vector: personal of the Carninci at
the RIKEN. The library was normalized and excised using
Cre recombinase. Plasmid cDNA library."
170 c 195 g 155 t 1 others
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/db_xref="taxon:7227"
/clone="RH56682"
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prlc-1"
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/dev_stage="Adult"
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Berkeley, CA
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Pred. No. 4.9e-57;
0; Mismatches 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 674;
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)., Frise, E., George
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RESULT 7
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AUTHORS
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KEYWORDS
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                                                                                                                                                                                                                                                                              Local
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                                                     CAAGTGAGGGGTATCAAGCGTCTATCTCTCTACGATGTGCCCCTACTTCAGCTTCGAGGGT
ATACCGTACGCCCAACCGCCAGTGGGTGAGCTTGAGATTTAAAGCACCCCAGCGACCAACA
                                                                         AAAGTGAAAGGCGTTAAACGTTTAACTGTGTACGATGATTCCTACTACAGTTTTTGAGGGT
                                                                                                                        AAAGTCCAGCAGTATCGCCAGTCGACCAATGAAACAGTTGTCGCCGACACGGAGTACGGC
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367; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA
Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Harvey,D., Brokstein,P., Hong,L.,
Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: http://www.fruitfly.org/EST, Plate: SD.167 row: A column: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2001)
Contact: Stapleton,
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1 (bases 1 to 676)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Drosophila
/db_xref="taxon:7227"
/clone="SD16705"
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173 c 194 g
                                                                                                                                                                                                                                                                                                                                                                                                                                   culture poT2"
                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: poT2; Site_1: EcoRI; fractionated cDNAs were directly lighter "
                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="DH5-alpha"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="SD Drosophila melanogaster Schneider L2
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Pred. No. 7.1e-57;
0; Mismatches 196;
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Best Local Similarity Matches 390; Conserv
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                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 660)
                                                                                                                                                                                                                                   Email: http://www.fruitfly.org/EST,
Plate: SD.220 row: F column: 7
High quality sequence stop: 546.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                        BDGP/HHMI Drosophila EST Project Unpublished (2001)
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BI639486.1 GI:15541696
                                                                                                                                                                                                                                                                                                                                                          Contact: Stapleton,
                                                                                                                                                                                                                                                                                                                                                                                                  Harvey,D., Brokstein,P., Hong,L.,
Lewis,S. and Rubin,G.M.
                                                                                                                                                                                                                                                                                                 One Cyclotron Rd, Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fruit fly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
                                                                          169
 Conservative
                                                                                                                                 /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="SD22067"
/clone="SD22067"
/clone_Lib="SD Drosophila melanogaster
culture pOT2"
/lab_host="DH5-alpha"
                                                                        /note-"Vector: pon2; Site_1: EcoRI; Site
fractionated cDNAs were directly ligated
plasmid cDNA library."
170 c 176 g 145 t
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BI614181.1
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Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Misra, S., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and Rubin
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                                                 BDGP/HHMI RH Drosophila
Unpublished (2001)
                                                                                      Phouanenavong, S.,,G.M.
                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila
1 (bases 1 to 673)
                                                                                                                                                                                                                                                                    fruit fly.
Drosophila
                                   Contact:
Berkeley
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Muscomorpha;
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BIG14443 672 bp mRNA linear EST 07-SEP-2001 RH43812.5prime RH Drosophila melanogaster normalized Head pFlc-1 Drosophila melanogaster cDNA clone RH43812 5:similar to alpha-Est7: FBan0001112 GO:[carboxyesterase (GO:0004091); carboxyesterase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GO:0004091)} located on: BI614443
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Unpublished (2001)
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One Cyclotron Rd, Berkeley, CA 94720,
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/dev_stage="Adult"
/lab_host="0H5-alpha TonA"
/note="Organ: head; Vector: pFlc1; Site_1: XhoI; Site_2: BamHI; Library was kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library."

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/db_xref="taxon:7227"
/clone="RH43812"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 13;
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                                 AAGTTTTTAAACTATCGTTTAACTACCAATGAAACGGTGGTAGCTGAAACTGAATATGGC
                                                                                            ATGAATAAGAACCTCGGCTTTGTGGAGCGCTTGCGGTGGCGCCTCAAAACCATCGAGCAT 169
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670 bp mRNA linear EST 11-JUL-2001 RE29491 Sprime RE Drosophila melanogaster normalized Embryo pFlc-1 Drosophila melanogaster cDNA clone RE29491 5 similar to alpha-Est7: FBan0001112 located on: 3R 84D5-84D5;: 04/12/2001, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: http://www.fruitfly.org/EST, plate: RE.294 row: H column: 7 High quality sequence stop: 534.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, B., Georg, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Misra, S., K., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Misra, S., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Mark, S., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Mark, S., Mark
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
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BI233202
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Lawrence Berkeley National Lab
Lawrence Berkeley National Lab
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168 c 194 g 155 t l others
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/db_xref="taxon:7227"
/clone="RE29491"
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/dev_stage="0-24 hours mixed
/lab_host="DH5-alpha TonA"
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Location/Qualifiers
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/clone_lib="GH Drosophila m
/sex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
/note="Organ: head; Vector:
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/db_xref="taxon:7227"
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                                  BDGP/HHMI Drosophila EST Unpublished (2001)
                        Contact:
                                                          Harvey, D., Brokstein, P., Lewis, S. and Rubin, G.M.
                                                                                Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
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GH09292.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH09292 Sprime similar to U51050: Drosophila melanogaster alpha esterase (aE7) gene, partial cds, aI109901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: http://www.fruitfly.org/EST,
Plate: 224 row: F column: 4
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62; Conservative
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quality sequence stop: 533.
Location/Qualifiers
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/db_xref="taxon:7227"
/db_cref="GH22464"
/clone="GH22464"
/clone_lib="GH Drosophila melanogaster head pOT2"
/sex="male and female"
/dev_stage="adult"
/dev_stage="adult"
/lab_host="DH5 - alpha"
/note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2: XhoI; Sized fractionated cDNAs were directly ligated into pOT2; plasmid cDNA library."
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                                                                  GGTGAAAATCATCGTGATATGTATGGTCCTGATTATTTCATTAAAAAGGATGTGGTGTTG
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ATTAACATACAATATCGTTTGGGAGCTCTAGGTTTTCTAAGTTTAAATTCAGAAGACCTT
                                               GGCGAGGCCAATCGGGAATGGTATGGCCCGGATTACTTTATGAAAGAAGATGTTGTTCTC
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Neoptera; Endopterygota; Diptera; Brachycera; Miscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.plate: 92 row: H column: 8
High quality sequence stop: 513.
Location/Qualifiers
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/db_xref="taxon:7227"
/clone="GH09292"
/clone_lib="GH Drosophila melanogaster head
/sex="male and female"
/tex=_stage="adult"
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/lab_host="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2: /note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2: /note="Organ: head; Vector: pOT2; Sized fractionated cDNAs were directly ligated into poT2. plasmid cDNA library."
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Berkeley, CA
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                                                                                                CAAGTGAGGGGTATCAAGCGTCTATCTCTCTACGATGTGCCCTACTTCAGCTTCGAGGGT
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 CCCTGGGATGGTGTGCGTGATTGTTGCAATCATAAAGATAAGTCAGTGCAAGTTGATTTT
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U51050: Drosophila melanogaster alpha esterase (aE7) gene, partial
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Lewis,S. and Rubin,G.M.
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Unpublished (2001)
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[ bases 1 to 646]
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/dev_stage="larvae-pupae"
/lab_host="DH5-alpha"
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CURRENT FILING DATE: 1998-05-20

EARLIER APPLICATION NUMBER: PCTAU96/00746

EARLIER FILING DATE: 1996-11-22

EARLIER APPLICATION NUMBER: AU 6751

EARLIER APPLICATION NUMBER: AU 6751

EARLIER FILING DATE: 1995-11-23

NUMBER OF SEQ ID NOS: 43

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 9

LENGTH: 1713

TYPE: DNA

ORGANISM: Lucilia cuprina
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Patent NO. 6235515
GEMERAL INFORMATION:
APPLICANT: Commonwealth Scientific and Industrial Rsrch.
APPLICANT: COMMONWEALTHION CARBOXYLESTERASE
FILE REFERENCE: Attorney Docket No. 6235515 50179-051
CURRENT APPLICATION NUMBER: US/09/068,960A
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GENERAL INFORMATION:
APPLICANT: Commonwealth Scientific and Industrial Rsrch.
FITTLE OF INVENTION: MALATHION CARBOXYLESTERASE
FILE REFERENCE: Attorney Docket No. 6235515 50179-051
CURRENT APPLICATION NUMBER: US/09/068,960A
CURRENT FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER FILING DATE: 1996-11-22
EARLIER FILING DATE: 1996-11-23
NUMBER OF SEQ ID NOS: 43
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APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org
TITLE OF INVENTION: MALATHION CARBOXYLESTERASE
TITLE OF INVENTION: MALATHION CARBOXYLESTERASE
TITLE REPERENCE: Attorney Docket No. 6235315 50179-051
CURRENT APPLICATION NUMBER: US/09/068,960A
CURRENT FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER FILING DATE: 1996-11-22
EARLIER APPLICATION NUMBER: AU 6751
EARLIER APPLICATION NUMBER: AU 6751
EARLIER APPLICATION NUMBER: AU 5751
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; MOLECULE TYPE: DNA (US-08-669-524-1
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Patent No. 5843758
GENERAL INFORMATION:
APPLICANT: RUSSELL, Robyn J.
                                                                                                                                                                                                                                                                                       TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/C
FILING DATE:
CLASSIFICATION: 435
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APPLICANT: NEWCOMB, Richard D.
APPLICANT: ROBIN, Geoffrey C.
APPLICANT: BOYCE, Thomas M.
APPLICANT: CAMPELL, Peter M.
APPLICANT: PARKER, Anthony G.
APPLICANT: CAKESHOTT, John G.
                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 703-684-1111
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NAME: Price, Robert L.
REGISTRATION NUMBER: 22,
REFERENCE/DOCKET NUMBER:
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MEDIUM TYPE: Floppy
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STREET: 99 Canal of
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
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AAGTTTTAAACTATCGTTTAACTACCAATGAAACGGTGGTAGCTGAAACTGAATATGGC
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CATGTTACAGGAGAAACACCAACAGCTGATAATTTTATGGATCTTTGCTCTCACATCTAT
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APPLICANN: Commonwealth Scientific and Industrial Rsrch. Org
ITITLE OF INVENTION: MALATHION CARBOXILESTERASE
FILE REFERENCE: Attorney Docket No. 6235515 50179-051
CURRENT APPLICATION NUMBER: US/09/068,960A
CURRENT FILING DATE: 1998-05-20
EARLIER APPLICATION NUBBER: FUT/AU96/00746
EARLIER FILING DATE: 1996-11-22
EARLIER APPLICATION NUMBER: AU 6751
EARLIER APPLICATION NUMBER: AU 6751
EARLIER FILING DATE: 1995-11-23
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 1713
TYPE: DNA
ORGANISM: Lucilla cuprina
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application Patent No. 6235515 GENERAL INFORMATION:
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RESULT 7
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                                                                                                                   EILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Price, Robert L.
REGISTRATION NUMBER: 22,685
REFERENCE/DOCKET NUMBER: 1451
                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,524
                                           TELEFAX: 703-684-1124 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                            TELEPHONE: 703-00.
TELEPHONE: 703-684-1124
THE TELEPHONE: 703-684-1124
TYPE: nuclei
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VENTION: ENZYME BASED
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PARKER, Anthony G
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NEWCOMB, Richard
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RESULT 8  Sequence 14, Application US/09068960A Patent NO. 6235515 GENERAL INFORMATION: APPLICANT: COMMONWEALTH Scientific and Industrial Rsrch. TITLE OF INVENTION: MALATHION CARBOXYLESTERASE FILE REFERENCE: Attorney Docket NO. 6235515 50179-051 CURRENT FILING DATE: 1998-05-20 EARLIER APPLICATION NUMBER: DCT/AU96/00746 EARLIER APPLICATION NUMBER: PCT/AU96/00746 EARLIER FILING DATE: 1996-11-23 EARLIER APPLICATION NUMBER: AU 6751 EARLIER APPLICATION NUMBER: AU 6751 EARLIER FILING DATE: 1996-11-23 NUMBER OF SEQ ID NOS: 43 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 14 LENGTH: 1710 TYPE: DNA ORGANISM: Musca domestica	y 1681 TCGATGTTTGAAAAACATAGAGATTTATTTTAG 1713 	1621 1621	y 1561 atggaaaatgtttcctgggatccaattaagaaatccgatgaagtatacaagtgtttgaat 	y 1501 ACTGGTATATGGATACAATTTGCCACCACTGGTAATCCTTATAGCAATGAAATTGAAGGT	1441 1441	y 1381 CGTAGTGGACGTGGTGTTAAGGGTGTTAGTCATGCTGATGAATTAACCTATTTCTTCTG	1321 1321	1261 1261	PARTICA CATGITACAGGAGAACACCAACAGCIGATAATITTATGGAICTITGCTCTCACAICTAT	1141 1141	2y 1081 CAAATGCCTATGCTTGTTAAGGAATTGGAAACTTGTGTCAATTTTGTGCCAAGTGAATTG	1021	
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	AAATTAAACAATGGGCAAGTATATTCGATAAAAAGAAGGAATTGTTT 1710	1664	рь
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1663	TCTATAAATGTTTAAATATCGGCGATGAATTGAAAGTTATGGATTTGCCAGAAATGGATA	1604	В
1663	TATACAAGTGTTTGAATATTAGTGATGAATGAATTGAAAATGATTGATGTGCCTGAAATGGATA	1604	Qy
1603	GCAATGATATAGCCGGCATGGAAAACCTCACCTGGGATCCCATAAAAAAAA	1544	Db
1603	GCAATGAAATTGAAGGTATGGAAAATGTTTCCTGGGATCCAATTAAGAAATCCGATGAAG	1544	Qy
1543	AAACCATTGAACGCATGGCATTTGGACGGAATTCGCCACCACCACCAAAACCATACA	1484	Дb
1543	AAACAATTGAACGTATGACTGGTATATGGATACAATTTGCCACCACTGGTAATCCTTATA	1484	Qy
1483		1424	DЪ
1483	TAACCTATTTCTTCTGGAATCAATTGGCCAAACGTATGCCTAAAGAATCGCCTGAATACA	1424	Qy
1423	ACCCCTATCGTATTATGCGTTTTGGCCGTGGCGTTAAAGGTGTAAGCCATGCCGATGAGC	1364	DЬ
1423	ATCCCTATCGTATTATGCGTAGTGGACGTGTTAAGGGTGTTAGTCATGCTGATGAAT	1364	Qy
1363	ACACAGCTGGCACTCCCATTTATTTGTATCGTTTCGATTTCGATTCCGAAGAAATTATTA	1304	рь
1363		1304	Qy
1303		1244	рь
1303	TTTGCTCTCACATCTATTTCTGGTTCCCCATGCATCGTTTGTTGCAATTACGTTTCAATC	1244	Qy
1243	CCATTGTGAAAAAGGCCCATGTGGATGGGGAAACACCTACTCTGGATAATTTTATGGAGC	1184	Db
1243	CTAAAATTAAAAAGGCTCATGTTACAGGAGAAACACCAACAGCTGATAATTTTATGGATC	1184	Qy
1183	ATGTGCCTTGGGAGTTGACAGTGAACGCAGTGCCCCGGAAACCCTTGGAGAGGGCTG	1124	DЬ
1183	TTGTGCCAAGTGAATTGGCTGATGTTGAACGCACCCCCCAGAGACCCTTGGAAATGGGTG	1124	Qy
1123	CCAAATCAATTGCCAAACAATATCCGGAGGTTGTAAAAGAGTTGGAATCCTGTGTGAATT	1064	ф
1123	TCACTTCAATTCTTAAGCAAATGCCTATGCTTAAGGAATTGGAAACTTGTGTCAATT	1064	Qy

RESULT 9
US-08-747-221B-51
Sequence 51, Application US/08747221B
Patent No. 6063610
GENERAL INFORMATION:
APPLICANT: Wishewski, Nancy
TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOSTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION NUMBER: US/08/747,221B
FILING DATE: No. 6063610ember 12, 1996
ATTORNEY/AGENT INFORMATION:

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Best Local 9
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Verser, Carol Talkington REGISTRATION NUMBER: 37,459 REFERENCE/DOCKET NUMBER: FC-1 TELECOMMUNICATION INFORMATION: TELEPHONE: 970/493-7272 TELEFAX: 970/484-9505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1584 nucleotides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29 AAGGTACTTTAAAAGGAAAAGAGCAAATTAGTGAAAAAGGAAATGTGTTCCATAGTTATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCGGTGCTGCCTCTACCCACTGATGTTAACCGAACAACTCGCGGTCTTTTCCATC
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                                                                       AAGCGATCTCACAAAGTGGAAGTGCTTTTAATCCTTGGGC
                                                                                                    GTGGTATACTAATGTCGGGTAATGCTATTTGTCCATTGGC 755
                                                                                                                                                                                                                                                                                                ACCTTAATGTGCCCGGTAATGCCGGCCTTAAAGATCAAGTCATGGCCTTGCGTTGGATTA
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                                                                                                                                        CAGGTGGTGCAAGTGTTCATTATTTGATGTTATCAGATCTTTCCAAAGGACTTTTTCATA
                                                                                                                                                                                                        AAAACAATATTGCATCCTTTGGTGGTGACCCCCAACAATGTGACTATTTTTGGAGAATCAG
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Similarity 56.2%;
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Sequence 52, Application Patent No. 6063610 GENERAL INFORMATION: APPLICANT: Silver, Ga

Gary

US/08747221B

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FILING DATE: No. 6063610ember 12, 199
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: EC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEPHONE: 970/493-7272
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Best Local Similarity
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TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: Windows 95 SOFTWARE: Wordperfect for Windows, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: cDNA
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                1436
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LENGTH: 1584 nucleotid
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                                                                                                                                                                                                                                                 CAAAAACATCAGAGAAATCACTTCTTCCAGTAATGGTATGGATACATGGAGGAGGCTTCT 1257
                                                                                                                                                                                                                                                                           ATTTATAACGGGCAAAGTGTGTGGGCTCAGAGGATTGTCTATACCTAAGTGTCTATACGA 355
                                                                                                                                                                                                                                                                                                                                                                                                            CAGAACCTTGGTCAGGTGTTCTTGATGCTAGTAAAGAAGGGAATAGTTGTAGATCAGTAC
                                                                                                         TGTTGATTAACATACAATATCGTTTTGGGAGCTCTAGGTTTTCTAAGTTTAAATTCAGAAG
                                                                                                                                                                 TCATGGGATCTGGAAATAGTGATATGTATGGTCCTGAATATTTGATGGATTATGGAATTG
                                                                                                                                                                                  TTATCGGTGAAAATCATCGTGATATGTATGGTCCTGATTATTTCATTAAAAAGGATGTGG
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  AA-----GCGCCTGGCAATGTTGGTTTGATGGACCAGGTTGAAGCTCTAAAATGGGTAA
                                                                                                                                                                                                                                                                                                                              ATTTTATTAAAAAAATTAAAGTAGGGGCTGAAGATTGTTTATACCTCAATGTCTATGTAC 1317
                                        ACCTTAATGTGCCCGGTAATGCCGGCCTTAAAGATCAAGTCATGGCCTTGCGTTGGATTA 595
                                                                                 TTCTGGTTACTTTCAATTATCGATTAGGTGTTTTGGGATTTTTGAACCTGGGAATAGAAG
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Pred. No. 2.3e-42;
0; Mismatches 274;
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US-09-005-051-51
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                                                                                                                                                                                      ; LOCATION: US-09-005-051-51
                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1082
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                                                                                                                                                                                                                                                                                                                                                                          RECISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Silver, Ga
APPLICANT: Wisnewski,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/747,221 FILING DATE: No. 6291222ember 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                             29
                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Verser, Carol Talkington REGISTRATION NUMBER: 37,459
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                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                  TOPOLOGY:
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              AGGGTATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCACCCCAGCGAC
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CTGGAATTCCATATGCCAAACCTCCTGTAGGTGATCTAAGATTTAAGCCACCTCAACCTG
                                                                                         ATGGCAAAGTGAAAGGCGTTAAACGTTTAACTGTGTACGATGATTCCTACTACAGTTTTG 175
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                                                                                                                      Score 179.6; [Pred. No. 2.3e: 0; Mismatches
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Patent No. 6291222
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                                                                                                                                               OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows,
CURRENT APPLICATION DATA:
APPLICATION NOTA:
                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/747,221
FILING DATE: No. 6291222ember 12,
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Silver, Gary W. APPLICANT: Wisnewski, Nancy
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                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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           NAME: Verser, Carol Talkington REGISTRATION NUMBER: 37,459
                                                                                                               CLASSIFICATION:
                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                 STATE:
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REFERENCE/DOCKET NUMBER:
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E: Heska Corporation
1825 Sharp Point Drive
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                                                                                                                                  Sequence 36, Application US/08747221B Patent No. 6063610 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1584 nucleotid
                      APPLICANT: Silver, Gary W.
APPLICANT: Wisnewski, Nancy
TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
CUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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   ADDRESSEE:
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Carol Talkington Verser, Ph.D. Heska Corporation
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Pred. No. 2.3e-42;
0; Mismatches 274;
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; LOCATION:
US-08-747-221B-36
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Matches 360; Conserv
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Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version
513 AAAACAATATTGCATCCTTTGGTGGTGACCCCAACAATGTGACTATTTTTGGAGAATCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Verser, Carol Talkington REGISTRATION NUMBER: 37,459 REFERENCE/DOCKET NUMBER: FC-1
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CITY: F
STATE:
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                  AAAATAATTGCGCCAACTTTGGTGGCAATCCCCGATAATATTACAGTCTTTGGTGAAAGTG
                                                                                      ACCTTAATGTGCCCGGTAATGCCGGCCTTAAAGATCAAGTCATGGCCTTGCGTTGGATTA 595
                                                                                                                                 TTCTGGTTACTTTCAATTATCGATTAGGTGTTTTTGGGATTTTTGAACCTGGGAATAGAAG
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                                                                                                                                                                                                                                                              CAAAAACATCAGAGAAATCACTTCTTCCAGTAATGGTATGGATACATGGAGGAGGCTTCT 338
                                                                                                                                                                                                                                                                                   ATTTTATTAAAAAAATTAAAGTAGGGGCTGAAGATTGTTTATACCTCAATGTCTATGTAC
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                                                                 AA-----GCGCCTGGCAATGTTGGTTTGATGGACCAGGTTGAAGCTCTAAAATGGGTAA
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Pred. No. 2.6e-42;
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RESULT 14
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Best Local Similarity
Matches 360; Conserv
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                                         1789
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REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970,493-7272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
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TOPOLOGY: lin
MOLECULE TYPE:
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ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
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NO. 6063610
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CAACACCCTGGGATGGTGCGTGATTGTTGCAATCATAAAGATAAGTCAGTGCAAGTTG 295
                                                                                                                                                                                                                                                      AAGGTACTTTAAAAGGAAAAGAGCAAATTAGTGAAAAAGGAAATGTGTTCCATAGTTATT 1910
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                                   ATTTTATTAAAAAATTAAAGTAGGGGCTGAAGATTGTTTATACCTCAATGTCTATGTAC 1730
                                                                    ATTTTATAACGGGCAAAGTGTGTGGCTCAGAGGATTGTCTATACCTAAGTGTCTATACGA 355
                                                                                                        CAGAACCTTGGTCAGGTGTTCTTGATGCTAGTAAAGAAGGGAATAGTTGTAGATCAGTAC 1790
                                                                                                                                                                               CTGGAATTCCATATGCCAAACCTCCTGTAGGTGATCTAAGATTTAAGCCACCTCAACCTG 1850
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                                                                                                                                                                                                                                                                                                                                           Score 179.6; DB 3
Pred. No. 2.6e-42;
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                                                                                                                                                                                                                              TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO:
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OPERATING SYSTEM: Windows 95
SOFTWARE: WordPorfect for Windows,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Silver, Ga
APPLICANT: Wisnewski,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1729 CAAAAACATCAGAGAAATCACTTCTTCCAGTAATGGTATGGATACATGGAGGAGGCTTCT 1670
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1669 TCATGGGATCTGGAAATAGTGATATGTATGGTCCTGAATATTTGATGGATTATGGAATTG 1610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  536
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                                                                                                                                                                                                                                                                                                                                                                              NAME: Verser, Carol Tal
REGISTRATION NUMBER: 37
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
                                          TOPOLOGY:
                                                                      STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Carol Talkington Verser, ADDRESSEE: Heska Corporation
                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGCGATCTCACAAAGTGGAAGTGCTTTTAATCCTTGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       633
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             GTGGTATACTAATGTCGGGTAATGCTATTTGTCCATTGGC 755
                                                                     CCGGTGCTGCCTCTACCCACTACATGATGTTAACCGAACAAACTCGCGGTCTTTTCCATC 715
                                                                                                                           AAAATAATTGCGCCAACTTTGGTGGCAATCCCGATAATATTACAGTCTTTTGGTGAAAGTG 655
                                                                                                                                                              AA-----GCGCCTGGCAATGTTGGTTTGATGGACCAGGTTGAAAATTGGGTAA 512
                                                                                                                                                                               ACCITAATGTGCCCGGTAATGCCGGCCTTAAAAGATCAAGTCATGGCCTTGCGTTGGATTA 595
                                                                                                                                                                                                                                                                                                                                   CAAAAACATCAGAGAAATCACTTCTTCCAGTAATGGTATGGATACATGGAGGAGGCTTCT 338
                                                                                                                                                                                                                                                                                                                                                                                         ATTTTATTAAAAAAATTAAAGTAGGGGCTGAAGATTGTTTATACCTCAATGTCTATGTAC 278
AAGCGATCTCACAAAGTGGAAGTGCTTTTAATCCTTGGGC 672
                                                       CAGGTGGTGCAAGTGTTCATTATTTGATGTTATCAGATCTTTCCAAAGGACTTTTTCATA 632
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Search completed: April 11, 2003, 08:51:10 Job time: 47.5118 secs

GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Published_Applications_NA:*

1: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

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1713
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

. 19	18'	17	16	15	14	13	12	11	10	9	8	7	6	5	4	ω	2	ш	Result No.
55.4	55.4	55.4	55.4	56.8	56.8	56.8	57.6	57.6	57.8	62.2	62.2	62.2	62.2	62.2	62.2	62.2	77.2	88.8	Score
3.2	3.2	3.2	3.2	ω . ω	ω . ω	ω .ω	3.4	3.4	3.4	3.6	3.6	3.6	3.6	3.6	3.6	3.6	4.5	5.2	Query Match
2428	2428	2087	1641	2484	2191	2191	4667	2508	657	2444	2416	2416	2416	2416	2381	1967	1611	1691	Query Match Length
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US-09-969-347-220	us-09-418-176-1	US-09-895-860-1	US-09-895-860-3	US-10-102-806-271	US-09-880-107-3854	US-09-954-531-1038	US-09-934-323-1	US-09-934-323-3	US-09-974-300-1107	US-09-893-519A-112	US-09-748-739A-16	US-09-748-739A-7	US-09-748-739A-5	US-09-748-739A-3	US-09-880-107-2271	US-09-748-739A-1	US-09-738-626-1254	US-10-083-590-13	ID
Sequence 220, App	Sequence 1, Appli	Sequence 1, Appli	Sequence 3, Appli	Sequence 271, App	Sequence 3854, Ap	Sequence 1038, Ap	Sequence 1, Appli	Sequence 3, Appli	Sequence 1107, Ap	Sequence 112, App	Sequence 16, Appl	Sequence 7, Appli	Sequence 5, Appli	Sequence 3, Appli	Sequence 2271, Ap	Sequence 1, Appli	Sequence 1254, Ap	Sequence 13, Appl	Description

21 55.4 3.2 3824 9 US-10-123-94-14 1 22 55.4 3.2 3824 9 US-10-123-94-541 24 55.4 3.2 3824 9 US-10-123-94-541 25 55.4 3.2 3824 9 US-10-123-94-541 25 55.4 3.2 3824 9 US-10-175-746-541 26 55.4 3.2 3824 9 US-10-176-918-541 28 55.4 3.2 3824 9 US-10-176-918-541 29 55.4 3.2 3824 9 US-10-176-918-541 29 55.4 3.2 3824 9 US-10-176-918-541 29 55.4 3.2 3824 9 US-10-227-884-209 31 55.4 3.2 3824 9 US-10-137-865-541 32 3824 9 US-10-137-865-541 32 3824 9 US-10-137-865-541 32 3824 9 US-10-137-865-541 32 3824 9 US-10-135-131-92 35 55.4 3.2 3824 9 US-10-140-474-541 36 55.4 3.2 3824 9 US-10-143-114-541 36 55.4 3.2 3824 9 US-10-123-1541 39 55.4 3.2 3824 9 US-10-123-1541 39 55.4 3.2 3824 9 US-10-123-1541 39 55.4 3.2 3824 9 US-10-123-160-22 41 39 55.4 3.2 3824 9 US-10-136-160-22 41 55.4 3.2 3824 9 US-10-036-160-22 54 55 54 3.2 3824 9 US-10-036-160-22 54 55 54 3.2 3824 9 US-10-036-160-22 54 55 54 3.2 3824 9 US-10-230-338 209 55 54 3.2 3824 9 US-10-123-262-541
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9 US-10-028-07 9 US-10-121-04 9 US-10-123-90 9 US-10-140-47 9 US-10-176-91 9 US-10-176-92 9 US-10-137-86 9 US-10-137-86 9 US-10-142-43 9 US-10-140-07 9 US-10-140-07 9 US-10-140-07 9 US-10-140-07 9 US-10-123-26 9 US-10-218-63 9 US-10-218-63 9 US-10-218-63 9 US-10-218-63
US-10-023-07 US-10-121-04 US-10-123-90 US-10-121-04 US-10-123-90 US-10-175-74 US-10-176-91 US-10-176-92 US-10-177-86 US-10-177-86 US-10-140-035-71 US-10-143-11 US-10-143-13-12 US-10-143-13-13-13-13-13-13-13-13-13-13-13-13-13
-10 - 028 - 07 - 07 - 07 - 07 - 07 - 07 - 07 - 0

## ALIGNMENTS

	AATCC 553	TTAATTACAGATTGAACGTCTTCGGTTTCCTGTCCATGAACACAAACAAAAATCC 553	Db 500 TTAATTACAGATTGAACGTCTTCGGTTTCCTO	
	TGTGC 547	AAGTT	Qy 488 TACAATATCGTTTGGGAGCTCTAGGTT	
	CACGT 499	GCCACGAGGACCTACACGGACCAGAATATTTGGTCACTAAGAATGTCATCGTCATCACGT	Db 440 GCCACGAGGACCTACACGGACCAGAATATTTGGTC	
	TAACA 487	- ≱	QY 428 ATCATCGTGATATGTATGGTCCTGATT	
	CTCCG 439	CACACCTTTACGGCCTATCCTGGTGTTCATACATGGTGGAGGATTTGCTTTCGGCTCCG 439	Db 380 CCACACCTTTACGGCCTATCCTGGTGT	
	TGAAA 427	CCGAAACTAAACGTCCCGTTTTAGTATACATACATGGTGGTGGTTTTATTATCGGTGAAA 427	Qy 368 CCGAAACTAAACGTCCCGTTTTAGTAT	
1;	6; Gaps	Pred. No. 7.2e-13; 0; Mismatches 177; Indels	Best Local Similarity 53.68; Pre Matches 211; Conservative 0;	
	•	re 88 8. DR 9. Length 1691.	л ж.	
			US-10-083-590-13	
			; TYPE: DNA	
			; LENGTH: 1691	
			; SOFTWARE: PatentIn Ver. 2.0	
			R OF SEQ ID NOS: 14	
		Ç	FILING DATE: EARLIER FILING	
	6 . 871	DATE: 1998-08-20	PRIOR FILING DATE: EARLIER FILING PRIOR ADDITION NUMBER - EARLIER	
	6,421	APPLICATION NUMBER: US 09/136,421	APPLICATION NUMBER: EARLIER	
	94	APPLICATION NUMBER: 09/256,694	æ	
		000,000	; CURRENT FILING DATE: 2002-02-27	
		083 F00	; FILE REFERENCE: 028722-207	
rs.	INSECT CELLS	MAMMALIAN AND	INVENTION: NON-SECRETED	
Į Į	SECRETION OF	IMPROVING THE EFFICIENCY OF		
			; GENERAL INFORMATION: ; APPLICANT: IATROU, KOStas	
		Ó	<pre>; Sequence 13, Application US/10083590 ; Publication No. US20030027257A1</pre>	
			RESULT 1 US-10-083-590-13	

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APPLICANT: OZAKI, AKIO

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

FILE REFERENCE: 249-125

FURRENT APPLICATION NUMBER: US/09/738,626

CURRENT FILING DATE: 2000-12-18

PRIOR APPLICATION NUMBER: JP 99/377484

PRIOR FILING DATE: 1999-12-16

PRIOR APPLICATION NUMBER: JP 00/159162

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 1254
LENGTH
                                                                                                                                                                                                                                                                                                                 Query Match 4.5%;
Best Local Similarity 50.2%;
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                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 16
TYPE: DNA
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414 TATTATCGGTGA----AAATCATCGTGATATGTATGGTCCTGATTATTTCATTAAAAAAGGA
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                                                G-----CCTGATTCCGAAGAAAAGCTTCCTGTTGTGGTGTATCTCCACGGCGGTTCCTT
                                                                 GTACTCCTGGACAGATAAGATTCGCGGTTCAGAAGACTGCCTTAACCTCGATGTCGTGCG
                                                                                                                                         TGATTTTATAACGGGCAAAGTGTGTGGCTCAGAGGATTGTCTATACCTAAGTGTCTATAC
                                                                                                                                                                        CANGAAATGGGACGGCGTGCGCGATTGCTCAATGTTCGGTGAAGTAGCTTCTCAGCCAAC
                                                                                                                                                                                                  AACACCCTGGGATGGTGTGCGTGATTGCTTGCA---ATCATAAAGATAAGTCAGTGCAAGT
                                                                                                                                                                                                                                    GGGAATTCCCTACGGCCGAAACACTGGCGGGAAAATATCGCTTCCGGGCACCCCGGCCCCGC
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OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
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US-09-748-739A-1
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1967
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09748739A Patent No. US20020119489A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         Matches 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lockridge, Oksana
APPLICANT: Watkins, Jeffry D.
TITLE OF INVENTION: Butyrylcholinesterase Variants and
TITLE OF INVENTION: Methods of Use
ELLE REFERENCE: P-IX 4143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/748,739A CURRENT FILING DATE: 2000-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Human Butyrylcholinesterase variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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   622
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AATCCCGATAATTACAGTCTTTGGTGAAAGTGCCGGTGCTGCCTC
                                                                                                          GGTGCCCTAGGATTCTTAGCTTT---GCCAGGAAATCCTGAGGCTCCAGGGAACATGGGT 670
                                                                                                                                            GGAGCTCTAGGTTTTCTAAGTTTAAATTCAGAAGACCTTAATGTGCCCGGTAATGCCCGGC
                                                                                                                                                                                 GATGGCAAGTTTCTGGCTCGGGTTGAAAGAGTTATTGTAGTGTCAATGAACTATAGGGTG
                                                                                                                                                                                                                GGTCCTGATTATTTCATTAAAAAAGGA---TGTGGTGTTGATTAACATACAATATCGTTTG 501
                                                                                                                                                                                                                                                        GTATTGATATGGATTTATGGTGGTGGTTTTCAAACTGGAACATCATCTTTACATGTTTAT
                                                                                                                                                                                                                                                                                           GTTTTAGTATACATACATGGTGGTGGTTTTATTATCGGTGAAAATCATCGTGATATGTAT 444
                                                                                                                                                                                                                                                                                                                                GAAGACTGTTTATATCTAAATGTATGGATTCCAGCACCTAAACC---AAAAAATGCCACT 493
                                    TTATTTGATCAACAGTTGGCTCTTCAGTGGGTTCAAAAAAATATAGCAGCCTTTGGTGGA
                                                                     CTTAAAGATCAAGTCATGGCCTTGCGTTGGATTAAAAATAATTGCGCCCAACTTTGGTGGC 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGAAGACCTTAATGTGCCCGCTAATGCCGGCCTTAAAGATCAAGTCATGGCCTTGCGTTG
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54.8%;
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Pred. No. 6e-06;
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; OTHER INFORMATION: Genbank Accession No. US20020142981A1 M16474
US-09-880-107-2271
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SEQ ID NO 2271
LENGTH: 2381
                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                   Sequence 3, Application US/09748739A Patent No. US20020119489A1
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Best Local Similarity
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TITLE OF INVENTION: Gene Expression Profiles
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
                                                         APPLICANT: Watkins, Jeffry D.
TITLE OF INVENTION: Butyrylcholinesterase Variants
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: P-IX 4143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
CURRENT APPLICATION NUMBER: US/09/748,739A CURRENT FILING DATE: 2000-12-06 NUMBER OF SEQ ID NOS: 31
                                                                                                                      APPLICANT: Lockridge, Oksana APPLICANT: Watkins, Jeffry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTGCCCTAGGATTCTTAGCTTT---GCCAGGAAATCCTGAGGCTCCAGGGAACATGGGT
                                                                                                                                                                                                                                                                                                              AATCCTAAAAGTGTAACTCTCTTTGGAGAAAGTGCAGGAGCAGCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGAGCTCTAGGTTTTCTAAGTTTAAATTCAGAAGACCTTAATGTGCCCGGTAATGCCGGC
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Pred. No. 6.7e-06;
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US-09-748-739A-3
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; LOCATION: (214)...(1935)
US-09-748-739A-5
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US-09-748-739A-5
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; LENGTH: 2416
; TYPE: DNA
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APPLICANT: Lockridge, Oksana
APPLICANT: Watkins, Jeffry
                                                                     Query Match
Best Local Similarity
Matches 190; Conserv
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/09748739A Patent No. US20020119489A1
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                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Watkins, Jeffry D.
TITLE OF INVENTION: Butyrylcholinesterase Variants
TITLE OF INVENTION: Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: P-IX 4143
                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0
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                  325 GAGGATTGTCTATACCTAAGTGTCTATACGAATAATCTAAATCCCGAAACTAAACGTCCC 384
481 GAAGACTGTTTATATCTAAATGTATGGATTCCAGCACCTAAACC---AAAAAATGCCACT 537
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                                                                   Score 62.2; DB 10 Pred. No. 6.8e-06; 0; Mismatches 148
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Pred. No. 6.8e-06;
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Sequence 7, Application US/09748739A
Patent No. US20020119489A1
GENERAL INFORMATION:
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; LOCATION: (214)...(1935)
US-09-748-739A-7
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
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Best Local :
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APPLICANT: Watkins, Jeffry D.
TITLE OF INVENTION: Butyrylcholinesterase Variants.
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: P-IX 4143
CURRENT APPLICATION NUMBER: US/09/748,739A
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION:
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    AATCCCGATAATATTACAGTCTTTGGTGAAAGTGCCGGTGCTGCCTC 668
                                                                   TTATTTGATCAACAGTTGGCTCTTCAGTGGGTTCAAAAAAATATAGCAGCCTTTGGTGGA
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Pred. No. 6.8e-06;
0; Mismatches 148;
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US-09-893-519A-112
; Sequence 112, Application US/09893519A
; Publication NO. US20030027243A1
; Publication...
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 2416
TYPE: DNA
ORGANISM: Homo sapiens
US-09-748-739A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-748-739A-16
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APPLICANT: Lockridge, Oksana
APPLICANT: Watkins, Jeffry D.
TITLE OF INVENTION: Butyrylcholinesterase Variants
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: P-IX 4143
CURRENT APPLICATION NUMBER: US/09/748,739A
CURRENT FILING DATE: 2000-12-06
                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                            APPLICANT: ANADYS PHARMACEUTICALS,
                                             APPLICANT:
                                                               APPLICANT
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                                                               HAQ,
LONG, Fan
DAVIDOV, Eugene
                                                                                                                                                              HARRIS, Sandra
KOMARNITSKY, Svetlana
                                                                                                                                                                                                                             BUURMAN, Ed T.
BRADLEY, John
                                                                                  SANDERSON, Karen
                                                                                                                                                                                                          DESILVA,
                                                                                                                                                                                                                                                                       MOORE, Jeffrey
                                                                                                      MOORE, Daniel
MCCOY, Melissa
                                                                                                                                               MENDILLO, Marc
                                                                                                                                                                                                                                                                                             THOMPSON,
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                                                               Tariq
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Pred. No. 6.8e-06;
0; Mismatches 148;
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Length Indels

2416; 9

Gaps

597

501 657

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622 715 Ş

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Matches

668 821

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; ORGANISM: Homo sapiens;
; ORGANISM: Homo sapiens;
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Human Genbank/NM_000055;
; DATABASE ENTRY DATE: 2001-02-03;
; RELEVANT RESIDUES: (1)..(2444)
US-09-893-519A-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-974-300-1107
                                                                                            NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1107
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1107, Application US/09974300 Patent No. US20020146721A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 3.6%;
Best Local Similarity 54.8%;
Matches 190; Conservative
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LENGTH: 2444
LENGTH: 657
TYPE: DNA
ORGANISM: Bacillus licheniformis
-09-974-300-1107
                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/974,300 CURRENT FILING DATE: 2001-10-05 PRIOR APPLICATION NUMBER: 09/680,598 PRIOR FILING DATE: 2000-10-06 PRIOR APPLICATION NUMBER: 60/279,526 PRIOR FILING DATE: 2001-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: ANTIFUNGAL COMPOUNDS AND METHODS OF FILE REFERENCE: 0342/16548-US2
CURRENT APPLICATION NUMBER: US/09/893,519A
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 60/215,164
PRIOR EILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 60/224,457
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 146
                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Methods For Monitoring Multiple Gene TITLE OF INVENTION: Expression FILE REFERENCE: 10085.500-US
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Berka, Randy M. APPLICANT: Clausen, Ib Gr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin version 3.1
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Pred. No. 6.8e-06;
O; Mismatches 148; Indels
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-934-323-3
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US-09-934-323-3
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; SEQ ID NO 3
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APPLICANT: CUITLS, ROTY A. J.
APPLICANT: CUITLS, ROTY A. J.
TITLE OF INVENTION: 33410, A NOVEL HUMAN CARBOXYLESTERASE
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
FILE REFERENCE: 10448-081001
                                                                                                                                                                                                                                                                         Best Local Similarity 54.2 Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09934323 Patent No. US20020150910A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/934,323
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/226,774
PRIOR FILING DATE: 2000-08-21
                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                           530 CAGAAGACCTTAATGTGCCCGGTAATGCCGGCCTTAAAGATCAAGTCATGGCCTTGCGTT
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851
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TCCAGAAGGCCATCGCCCAGAGTGGCACCGCCATTT
                              TCCATCGTGGTATACTAATGTCGGGTAATGCTATTT 745
                                                                 CCGGGGCAGGGGCCTCCTGCGTCAACCTTCTGATCCTCTCCCACCATTCAGAAGGGCTGT
                                                                                     AAAGTGCCGGTGCTGCTCTACCCACTACATGATGTTAACCGAACAACTCGCGGTCTTT
                                                                                                                                                         GGATTAAAAATTGCGCCAACTTTGGTGGCAATCCCGATAATATTACAGTCTTTGGTG
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54.2%;
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                                                                                                                                                                                                                                                                                       Score 57.6;
Pred. No. 0
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Pred. No. 4.5e-05;
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RESULT 12 US-09-934-323-1

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; LOCATION: (420)...(2924)
US-09-934-323-1
                                   ; TYPE: DNA
; ORGANISM: HOMO
US-09-954-531-1038
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APPLICANT: CUITLS, ROTY A. J.
APPLICANT: CUITLS, ROTY A. J.
TITLE OF INVENTION: 33410, A NOVEL HUMAN CARBOXYLESTERASE
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
FILE REFERENCE: 10448-081001
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/226,774
PRIOR FILING DATE: 2000-08-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 3.4%;
Best Local Similarity 54.2%;
Matches 117; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                            SEQ ID NO 1038
Query Match
                                                                                                                                                                             PRIOR APPLICATION NUMBER: US/60/234,009
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,034
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,509
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US/60/234,567
                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cancer TITLE OF INVENTION: Gene Sets FILE REFERENCE: 689290-77 CURRENT APPLICATION NUMBER: US/09/954,531 CURRENT FILING DATE: 2002-05-02 CURRENT FILING DATE: 2002-05-02
                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US/60/233,133
PRIOR FILING DATE: 2000-09-18
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                                                                                                                                                                PRIOR FILING DATE: 2000-09-22
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ORGANISM: Homo sapiens
FEATURE:
                                                                                     LENGTH: 2191
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                                                                                                                             PatentIn version 3.0
                                                      sapiens
   3.38;
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Pred. No. 0.00015;
0: Mismatches 99;
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FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOCTWARE: PATENTIN VET. 2.1
SEQ ID NO 3854
LENGTH: 2191
TYPE: DNA
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US-09-880-107-3854
                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens ; FEATURE: OTHER INFORMATION: Genbank Accession No. US20020142981A1 Y09616 US-09-880-107-3854
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                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 215; Conserv
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APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles
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CGTCCCGTTTTAGTATACATACATGGTGGTGGTTTTATTATCGGTGAAAATCATCGTGAT 438
                                                                      CTGCCGGTGATGGTGGATCCACGGTGGTGCGCTTGTTTTTG--GCATGGCTTCCTTGT
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0; Mismatches 177;
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Pred. No. 0.
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RESULT 15
US-10-102-806-271
; Sequence 271, Application US/10102806
; Publication No. US20030054421A1
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Best Local Similarity
Matches 215; Conserv
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CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/925,298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
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## SUMMARIES

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SM Unclassified.

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E 1 (bases 1 to 1713)

RS Russell, R. Joyce., Newcomb, R. David., Campbell, P. Malcolm., R. Robin, G. Charlesde. Quetteville., Claudianos, C., Smyth, K.-Boyce, T. Mark., Oakeshott, J. Graham. and Brownlie, J. Colin Malathion carboxylesterase

Malathion carboxylesterase

NAL Patent: US 6235515-A 9 22-MAY-2001;

Location/Qualifiers

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             GAAGAGCGTACAAATAAGGTCATGTTTCCTTTTGGTCCCACTGTTGAGCCATATCAGACC
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Sequence
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AR153438.
                                                1 (bases 1 to 1713)
Russell,R.Joyce., Newcomb,R.David., Campbell,P.Malcolm., Robin,G.Charlesde.Quetteville., Claudianos,C., Smyth,K.-A., Boyce,T.Mark., Oakeshott,J.Graham. and Brownlie,J.Colin. Malathion carboxylesterase Patent: US 6235515-A 1 22-MAY-2001;
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Sequence
AR153440
AR153440.
                l (bases 1 to 1713)
Russell,R.Joyce., Newcomb,R.David., Campbell,P.Malcolm.,
Russell,R.Joyce., Newcomb,R.David., Campbell,P.Malcolm.,
Robin,G.Charlesde.Quetteville., Claudianos,C., Smyth,K.-A.,
Boyce,T.Mark., Oakeshott,J.Graham. and Brownlie,J.Colin.
Malathion carboxylesterase
Patent: US 6235515-A 5 22-MAY-2001;
Location/Qualifiers
1. .1713
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Unclassified
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Sequence 1
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AR062837.1
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Russell.R.Joyce., Newcomb,R.David.,
Boyce.T.Mark., Campbell,P.Malcolm.,
Oakeshott,J.Graham. and Smyth,K.-A.
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                                                                                                           Patent:
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JOURNAL MEDLINE PUBMED REFERENCE AUTHORS

Insect Biochem. 97215578 9061925

Mol.

Biol. 27 (1),

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3 (bases 1 to 2240)
Newcomb,R.D., Campbell,P.M., Ollis,D.L., Cheah,E., Russell,R.J.
Oakeshott,J.G.
A single amino acid substitution converts a carboxylesterase to organophosphorus hydrolase and confers insecticide resistance or

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8799740 2 (bases 1 to 2240) 2 (bases 1 to 2240) Newcomb,R.D., Campbell,P.M., Russell,R.J. and Oakeshott,J.G. CDNA cloning, baculovirus-expression and kinetic properties of the esterase, E3, involved in organophosphorus resistance in Lucilia	nes associated w cuprina )	nsec a; N		e resistance, complete cds. 336070	U56636 2240 bp mRN Cilia cuprina alpha esterase (LcaE7)	TCGATGTTTGAAAAACATAGAGATTTATTTTAG 1713	TCGATGTTTGAAAAACATAGAGATTTATTTTAG 1713	ATTAGTGACGAATTGAAAATGATTGATGTGCCTGAAATGGATAAGATTAAACAATGGGAA 1680	ATTAGTGATGAATTGAAAATGATTGATGTGCCTGAAATGGATAAGATTAAACAATGGGAG 1680	ATGGAAAATGTTTCCTGGGATCCAATTAAGAAATCCGACGAAGTATACAAGTGTTTGAAT 1620	ATGGAAAATGTTTCCTGGGATCCAATTAAGAAATCCGATGAAGTATACAAGTGTTTGAAT 1620	ACTGGTATATGGATACAATTTGCCACCACTGGTAATCCTTATAGCAATGAAATTGAAGGT 1560	ACTGGTATATGGATACAATTTGCCACCACTGGTAATCCTTATAGCAATGAAATTGAAGGT 1560	ANTCAATTGGCCAAACGTATGCCTAAAGAATCGCGTGAATACAAAACAATTGAACGTATG 1500	AATCAATTGGCCAAACGTATGCCTAAAGAATCGCGTGAATACAAAACAATTGAACGTATG 1500	CGTAGTGGACGTGGTTAAGGGTGTTAGTCATGCTGATGAATTAACCTATTTCTTCTGG 1440	CGTAGTGGACGTGGTGTTAAGGGTGTTAGTCATGCTGATGAATTAACCTATTTCTTCTGG 1440	GTCTACTTGTATCGCTTCGACTTTGATTCGGAAGATCTTATTAATCCCTATCGTATTATG 1380	GTCTACTTGTATCGCTTCGACTTCGATTCGGAAGATCTTATCAATCCCTATCGTATTATG 1380	TICTGGTTCCCCATGCATCGTTTGTTGCAATTACGTTTCAATCACACCTCCGGTACACCC 1320	TTCTGGTTCCCCATGCATCGTTTGTTGCAATTACGTTTCAATCACACCTCCGGTACACCC 1320	CATGTTACAGGAGAACACCAACAGCTGATAATTTTATGGATCTTTGCTCTCACATCTAT 1260	CATGTTACAGGAGAAACACCCAACAGCTGATAATTTTATGGATCTTTGCTCTCACATCTAT 1260	

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confer alternative types of organophosphorus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (24-APR-1996) Richard D. Newcomb, Molecular Genetics, HortResearch, Private Bag 92 169, Auckland, New Zealand Location/Qualifiers
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VKRLTVYDDSYYSFEGIPYAQPBVGELRFKAPQRFTPMDGVROCCNHKDKSVQVDFIT
GKVCGSEDCLYLSVYNNLNPETKRPVLVYIHGGGFIGEURRDMYGPDYFIKRDVLL
INIQYRLGALGFLSLNSEDLNVFGNAGIKDQVMALRWIKNNCANFGGNPDNITVFGES
AGAASTHYMMLTEQTRGLFHRGILMSGNAICPWANTQCQHRAFTLAKLAGYKGEDNNK
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TAWGNSIPTMMGNTSYEGLFFTSILKQMPMLVKELETCVNFVPSELADAERTAPETLE
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1140	081 CAAATGCCTATGCTTGTTAAGGAATTGGAAACTTGTGTCAATTTTGTGCCAAGTGAATTG	ОУ 10
1377	18 ATACCCACTATGATGGGTAACACTTCATATGAGGGTCTATTTTTCACTTCAATTCTTAA	, pb 13
1080	21 ATACCCACTATGATGGGTAACACTTCATATGAGGGTCTATTTTT	Qy 10
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1257	01 GAAGAGGGTACAATAAGGTCATGTTTCCTTTTGGTCCCACTGTTGAGCCATATCAGACC 	, Qу 9
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957	98 AATTGCGCCAACTTTGGTGGCAATCCCGATAATATTACAGTCTTTGGTGAAAGTGCCGGT	Db 8
660	01 AATTGCGCCAACTTTGGTGGCAATCCCGATAATATTACAGTCTTTGGTGAAAGTGCCGGT	Qy 6
897	41 AATGTGCCCGGTAATGCCGGCCTTAAAGATCAAGTCATGGCCTTGCGTTGGATTAAAAAT	Db 8
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Query Match 97.9%; Score 1676.6; DB 6; Length 1713; Best Local Similarity 98.0%; Pred. No. 0; Matches 1679; Conservative 0; Mismatches 34; Indels 0; Gaps 0;  ATGAATTTCAACGTTAGTTTGATGGAGAAATTAAAATGGAAGATTAAAATGCATTGAAAAT 60  11111111111111111111111111111111111	REFERENCE 1 (bases 1 to 1713)  AUTHORS RUSSEll,R.Joyce., Newcomb,R.David., Robin,G.Charlesde.Quetteville.,  Boyce,T.Mark., Campbell,P.Malcolm., Parker,A.Gerard.,  Oakeshott,J.Graham. and Smyth,KA.  TITLE Enzyme based bioremediation JOURNAL Patent: US 5843758-A 2 01-DEC-1998; FEATURES Source 1. 1713  BASE COUNT 506 a 299 c 363 g 515 t 30 others	RESULT 8 AR062838 LOCUS AR062838 LOCUS AR062838 DEFINITION Sequence 2 from patent US 5843758. ACCESSION AR062838 VERSION AR062838.1 GI:5990529 KEYWORDS SOURCE ORGANISM Unknown.	Db 1858 ATGGAAAATGTTTCCTGGGATCCAATTAAGAAATCCGAACGAA	Qy 1441 AATCAATTGGCCAAACGTATGCCTAAAGAATCGCGTGAATACAATTGAACGTATG 1500	1558 TCTGGTTCCCATGCATCGTTGTGTGTATTAGGTTTCAATCCACACCTCCGGTATAACCCC  1321 GTCTACTTGTATCGCTTCGACTTCGATTCGAATCCAATCCAATCCCTATCGTATTATG	Db 1378 CAAATGCCTATGCTTGTTAAGGAATTGGAAACTTTGTGCCAAGTGAATTG 1437  Qy 1141 GCTGATGCTGAACGCACCGCCCCAGAGACCTTGGAAATGGGTGCTAAAATTAAAAAGGCT 1200
Oy 1021 ATACCCACTATGATGGGTAACACTTCANINGAGGGTCTATTTTTCACTTCACTTCACATTCATAGG 1080	841 TTTCTTATGAAAGCCAAGCCACAGGATTTAATAAAACTTGAAGGCAAAAAGTTTTAACTCTA 841 TTTCTTNTGAAAGCCAAGCCACAGGATTTAATAAAACTTGAGGAAAAAAGTTTTAACCTCTA 901 GAAGAGCGTACAAATAAGGTCATGTTTCCTTTTGGTCCACTGTTGAGCCCATATCAGACC 111111111111111111111111111111111		Oy 541 AATGTGCCCGGTAATGCCGGCCTTAAAGATCAAGTCATGGCCTTGCGTTGGATTAAAAAT 600	QY 301 CTARACICCGAAACITACAGICCCGTTTTAGTATACATIGGTGGTGTTTATTATC 420	241 CCCTGGGATGGTGTGCCCGATTGTTGTATAAAGATAAGTCAGTGCAAGTTGATTTT	Qy 61 AAGTTTTTAAACTATCGTTTAACTACCAATGAAACGGTGGTAGCTGAAACTGAATATGGC 120

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                                                                                                                                             Claudianos, C., Ru
Direct Submission
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The same amino acid substitution in orthologous esterases organophosphate resistance on the house fly and a blowfly Insect Blochem. Mol. Biol. 29 (8), 675-686 (1999)
                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Ptérygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Nuscoldea; Muscidae; Musca
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/strain="Rutgers Diazinon-R (R+)"
/db_xref="taxon:7370"
/chromosome="II"
 /gene="MdaE7"
               /dev_stage="4
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                                                                   AATGTGCCCGGTAATGCCGGCCTTAAAAGATCAAGTCATGGCCTTGCGTTGGATTAAAAAT
                                                                                                      GTAACCGTGCAATATCGTTTGGGTGTGTTGGGTTTCCTTAGCCTGAAATCGGAAAATCTC
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                                                    AATGTCCCCGGCAACGCTGGCCTCAAGGATCAAGTAATGGCCTTGAGATGGGTCAAGAGT
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/KRMTVYDDSYYSFESI PYAKPPVGELRFKAPQRPVPWEGVRDCCGPANRSVQTDFIS
GKPTGSEDCLYLNVTINDLNPDKKRPVEFIHGGDF IEGANRIWFGGPDYFMKKPVVL
VTVQYRLGVLGFLSLKSENLNVPGNAGLKDQVMALRRVKSNIANFGGDPUNITVFGES
AGGASTHYMMITEQTRGLFHRGIMMSGNSCSWASTECQSRALTMAKRVGYKGEDNEX
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RAAIVKKAHVDGETPTLDNFMELGSYEYFLFPWHRFLQLRFWHTAGTPIYLYRFDFDS
BEIINPYRIMREGRGVKGVSHADELTYLFWNILSKRLPKESREYKTIERMVGIWTEFA
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/EC_number="3.1.1.1"
/note="mutant ali-esterase; similar
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/protein_id="AAD29685.1"
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                                                                                                                       ATGGAAAATGTTTCCTGGGATCCAATTAAGAAATCCGATGAAGTATACAAGTGTTTGAAT 1620
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                                                                                                                                                             GTTGGCATTTGGACGGAATTCGCCACCACCGGCAAACCATACAGCAATGATATAGCCGGC 1776
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                                                                                                          ATGGAAAACCTCACCTGGGATCCCATAAAAAAATCCGATGATGTCTATAAATGTTTAAAT
                                                    ATCGGCGATGAATTGAAAGTTATGGATTTGCCAGAAATGGATAAAATTAAACAATGGGCA 1896
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Insects Research Laboratory, 2700
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Direct Submission
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vkrltvyddsfysfegipyakpevgelrekaporpyphogvadocchaashsvogtdfig
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/note="similar to I
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TTGNPYSPEINGMENTTWDSLKKSDEVYKCMNIGDELKFIDLPEMEKLKVWQSVFNKK
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/strain="Camp Cooley 4/97"
/sub_species="irritans"
/db_xref="taxon:75445"
/clone="HF41CC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="alpha E7 esterase"
/protein_id="AAF14517.1"
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Russell,R.Joyce., Newcomb,R.David., Campbell,P.Malcolm.,
Robin,G.Charlesde.Quetteville., Claudianos,C., Smyth,K.-A.,
Boyce,T.Mark., Oakesbott,J.Graham. and Brownlie,J.Colin.
Malathion carboxylesterase
Patent: US 6235515-A 14 22-MAY-2001;
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This clone was sequenced as part of a high-throughput process to sequence clones from Drosophila Gene Collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular cDNA clone. However, there are artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAs, and reverse transcriptase errors that result in single base changes. For further information about this sequence, including its location and relationship to other sequences, please visit our Web site (http://fruitfly.berkeley.edu) or send email to contain/Qualifiers
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Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 2017)

Stapleton,M., Brokstein,P., Hong,L., Agbayani,A., Carlson,J.,

Champe,M., Chavez,C., Dorsett,V., Farfan,D., Frise,E., George,R.,

Gonzalez,M., Guarin,H., Li,P., Liao,G., Miranda,A., Mungall,C.J.,

Nunco,J., Pacleb,J., Paragas,V., Park,S., Phouanenavong,S., Wan,K.

Yu,C., Lewis,S.E., Rubin,G.M. and Celniker,S.
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AY051473
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Berkeley Drosophila Genome Project Lawrence Berkeley National Laboratory Berkeley, CA 94720
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h 39.7%;
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VTIQYRLGALGEWSLKSPELNVPGNAGLKDQTHNPYRIAKLUGYKGEDND
AGGASTHYMMLTDQTQGLFHRGILQSGSAICPWAYNGDITHNPYRIAKLUGYKGEDND
KDVLEFLQNVKAKDLIKVERVLTLEERNNKIMFAFGPSLEPFSTPECVISKPPKEMM
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KTAWSNSIPMFIGNTSYEGLLMVPEVKLMPQVLQOLDAGTPFTFKELLATEPSKEKLD
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SEBLIFYRIMKLGRGVKGVSHADDLSYGPSSLLARRLPKESREYRNIERTVGIWTQF
SEBLIFYRIMKLGRGVKGVSHADDLSYGPSSLLARRLPKESREYRNIERTVGIWTQF
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/note="alignment with genomic scaffold
/db_xref="FLYBASE:FBgn0015575"
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      GAGTCGATGTTTGAAAAACATAGAGATTTATTTT
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Berkeley, CA 94720

Berkeley, CA 94720

This clone was sequenced as part of a high-throughput process to sequence clones from Drosophila Gene Collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular cDNA clone. However, there are artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAs, and reverse transcriptase errors that result in single base changes. For further information about this sequence, including its location and relationship to other sequences.
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Sequence submitted by:
Berkeley Drosophila Geno
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AY121675.1
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Location/Qualifiers
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                                                                                                           /GL_XTEGF="FLYBASS: FBGn0015576"
//GL_XTEGF="FLYBASS: FBGn0015576"
/KRQSIYSNNYYSFEGIPFAKDOWRIALNYVKFKTNOORLRSNDKVIADTVYGKVKG
VKWQSIYSNNYYSFEGIPFAKDOVGELRFKAPVEPEHWSDVRACTHVRAKPCQVNIVL
KOVQGSEDCLYLNVYTRELHPHRPLFULVMIYGGGFQMEBASRDLYSPDY IMMEHVVI
VVISYRLGALGFLSLADEELDVPGNAGIKDQVWALRWVKNCQFFGGDPDNITVFGES
AGGASTHYMMLTDQAKGLFHKTIINGSSALAPWAQTFTHINMPYRLAQATGYTGDAND
RDIFAHLKKCRASSMLKVAEDIITMEERHQRLTMFSGFTIENLAPQDAHCYIFKSPLEM
MRDCWGNSIPMYIGGNSFGGLLMFBEVNKWPELLCQLGDFIEPYLTPHCVIFKSPLEM
GKKVRELYFGDRTFGRKTILEYSDLFSYKYFWHGIHRTLLSRAHHAPLAPTFLYRFDF
GKKVRELYFGDRTFGRKTTCHADDLSYLFYNAAAKKLKRRTAEFKTIKRLYSMVVHF
                         AISGDPNIPMVCQDEKEQPRGAWLPISKDDKVFQCLNISHDVHVIDLPEAEKLRLWDC
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/protein_id="AAM52002.1"
/db_xref="GI:21464398"
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/strain="y; cn bw sp"
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AAGGAATTGGAAACTTGTGTCAATTTTGTGCCAAGTGAATTGGCTGATGCTGAACGCACC 1158
                                                                                                                                AAACATCCTCGGGAAATGGTTAAAACTGCTTGGGGTAATTCGATACCCACTATGATGGGT 1038
                                                                                                                                                                                   ACCATGTTCAGCTTTGGACCCACCATCGAGCCCTATTTGACTCCTCATTGTGATTCCC
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                                                                                                                                        Robin,C., Medveczky,K.M., Russell,R.J. and Duplication and Divergence of the genes of cluster of Drosophila melanogaster J. Mol. Evol. (1996) In press
                                                                         Submitted (11-MAR-1996) Charles Robin, Biotechnology, Entomology, Clunies Ross Street, Canberra, ACT 2601, A Location/Qualifiers
                                                                                                                                                                                                          Drosophila melanogaster.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 2820)
                                                                                                                       Direct Submission
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/map="84D3"
/note="Yac clone DY219"
                                       /organism="Drosophila
/db_xref="taxon:7227"
                                                 melanogaster"
                                                                                                                                                                                                                                                                                                                        (aE7): gene,
                                                                                                                                                                                                                                            Insecta; Pterygota;
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the alpha-esterase
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                                                                                                                                                                           TGGTGCTTTGGGTAATCTACTGTGTGCGTATGCGCAATATTTTGACTAAACATTATTGTA
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                                                                         CCTACACAGGATTTATGAGTCTTAAGTCCCCCGAGCTAAATGTACCAGGAAATGCTGGCC
                                                                                                            ----AGGTTTTCTAAGTTTAAATTCAGAAGACCTTAATGTGCCCGGTAATGCCGGCC
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                                                                                                                                                                                                                                                                                                                   GTATGGTCCTGATTATTTCATTAAAAAGGATGTGGTGTTGATTAACATACAATATCGTTT
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/Product-"alpha esterase"
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SPELNVPGNAGLKDQVLALKWIKNNCASFGGDDNCITVFGESAGGASTHYMMITDO7Q
GLEHRGILOSGSALCPMAYNGDITHNPYRIAKLVGYKKEDNOKDVLEFQAVKAKDLI
RVEENVLTLEERMNKIMFRFGPSLEPFSTPECVISKPPKEMMKTAWSNSIPMFIGNTS
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TPONYMDLCSIYYFVFPALRVHSRHAYAAGAPVYFYRYDFDSEELIFPYRIMRMGRG
VKOVSHADDLSYQFSSLLARRLPKESREYRNIERTVGIWTQFAATGHPYSEKINGMDT
LTIDPVRKSDEVIKCLMISDDLKFIDLPEWPKLKVWESLYDDNKDLLF"
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                                                                      CGAAGGAAAGTCGCGAGTACAGGAACATCGAACGAACCGTGGGCATCTGGACCCAGTTTG
                                                                                            CTAAAGAATCGCGTGAATACAAAACAATTGAACGTATGACTGGTATATGGATACAATTTG
                                                                                                                                        GTGTTAGTCATGCTGAATGAACTTAACCTATTCTTCTGGAATCAATTGGCCAAACGTATGC
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36181
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                                                           TACAGTTTTGAGGGTATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCA
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GTGTACACCAACAATGTGAGTAATTCTATTAACTTGTGTACATAAAACATCGTTAAAAACC 36122
                             GTCTATACGAATAAT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence was identified as CDM:1021345
For further information on this sequence e-
* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is

* the accession number will be preserved.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
Eukaryota; Endopterygota; Diptera; Brachycera; Musco
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 57335)
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AC015272
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11816 c 11532 g 16881 t
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35042	GCÁCCCCAG	35101
1242	CAGCTGATAATTTT	1218
35102	COCCCMMANACTIGNAMAINGUTECTHAMATTAMAMAGGCTCATGTTACAGGAGAAACTAAAAGAAACTAGATTCGTGGAGTGCACAGATTCGAGATGTTCATCGCACTGGCTCAGA	35161
51	CAGCTTGATGCTGGCACACCTTTCATTCCCAAAGAATTGCTG	n N
1157	GCTGAACG	1098
Ü	TTCTTTCAATAAGTAAATTTAATTTCACAGAGGTAAAGCTTATGCCGCAGGTGCT	28
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1058 35282	ACACTTCATATGAGGGTCT	1040 35341
1039 35342	AACATCCTCGGGAAATGGTTAAAACTGCTTGGGGTAATTCGATACCCACTATGATGGGTA	980 35401
G	TAATGTTTGCCTTTGGCCCATCCCTGGAACCATTCTCCACGCCCGAATGTGTGATATCCA	35461
979	CATGTTTCCTTTTGGTCCCACTGTTGAGCCATATCAGACCGCTGATTGTGTCTTACCC	920
919 35462	CACAGGATTTAATAAAACTTGAGGAAAAAGTTTTAACTCTAGAAGAGCGTACAAATAAGG	860 35521
859 35522	CCGGCTATAAGGGTGAGGATAATGATAAGGATGTTTTTGGAATTTCTTATGAAAGCCAAGC	800 35581
799 35582	TTTGTCCATTGGCTAATACCCAATGTCAACATCGTGCCTTCACCTTAGCCAAATTGG	743 35641
742 35642	TGTTAACCGAACAACTCGCGGTCTTTTCCATCGTGGTATACTAATGTCGGGTAATGCTA	683 35701
682 35702	ATCCCGATAATATTACAGTCTTTGGTGAAAGTGCCGGTGCCTCCACCACCACTAQATGA	623 35761
622 35762	TTAAAGATCAAGTCATGGCCTTGGGTTGGATTAAAAATAATTGCGCCAACTTTGGTGGCA	563 35821
562 35822	AGGTTTTCTAAGTTTAAATTCAGAAGACCTTAATGTGCCCGGTAATGCCGGCC	510 35881
35882	TGGGGCTTTGGGTAATCTACTGTGTGCGCAATATTTTTGACTAAACATTATTGTA	35941
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440 36002	TCCCGTTTTAGTATACATACATGGTGGTGGTGTTTATTATCGGTGAAAATCATCGTGATAT	381 36061
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Search completed: April 11, 2003, 06:03:00 Job time: 3045.03 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 1.0
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                    OP-sensitive ester LC-alpha-E7 malath OP-resistant ester OP-resistant ester OP-resistant ester OP-resistant ester OP-resistant ester OP-resistant ester Md-alpha-E7 gene.
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Md-alpha-E7 gene.
Drosophila melanog
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AAD21169	AAV40743	AAV40767	ABL01946	ABL02029	ABL01942	AAD21174	AAV40755	AAV40754	AAV40757	AAV40756	AAV40765	AAV40764	ABL01858	ABL19064	ABL01945	AAV40763	AAV40762	ABL02100	ABL02098	ABL02080	ABL02102	ABL01943	ABL04688	ABA90480	ABL07668	ABL10332	ABL01947	ABL02101	ω	ABL01859	0	ABL04689	ABL02099	ABL02066	ABL02081
Ctenocephalides fe	C. felis esterase,	C. felis esterase		Drosophila melanog	Drosophila melanog	tenoceph	felis	felis		felis	felis	felis esterase		Drosophila melanog	rosophil	C. felis esterase,	ເກ																		Drosophila melanog

## ALIGNMENTS

RESULT 1 AAQ91561 Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG; Parker AG, Robin GC, Russell RJ, Smyth K; CDS 13-JAN-1994; 13-JAN-1995; 20-JUL-1995 WO9519440-A1 Esterase; E3; bioremediation; organophosphate; carbamate; insecticide; pesticide; water decontamination; meat decontamination; OP-sensitive esterase E3 Lc743 clone 22-DEC-1995 AAQ91561; AAQ91561 standard; cDNA; 1713 BP (CSIR ) COMMONWEALTH SCI & IND RES ORG. Lucilia cuprina (first entry) 94AU-0003347 95WO-AU00016 Location/Qualifiers 1..1713 /\*tag= a

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                                                                                                                                                                                                                                                                                                                            cDNA from organophosphate (OP)-sensitive L. cuprina pupa cDNA library was amplified using cluster-specific esterase primers. Isolated clone LC743, a probable full-length cDNA, was expressed using a baculovirus vector in insect cells and shown to encode an OP-susceptible E3 esterase, useful in bioremediation.
                                                                                                                                                                                                                                                                                                                                                                               Pure E3 esterase from eliminate residues of
                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB;
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DB; AAR78142.
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                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                             Conservative
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  of organo:phosphate and carbama
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Pred. No. 0;
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RESULT 2
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ID AAT6
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AC AAT6
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AC AAT6
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AAT68596

standard;

DNA;

1713 BP

08-AUG-1997

(first

entry)

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Query Match
Best Local Similarity
                                                                                            DNA molecule Lc743 (AAT68596) codes for an esterase (AAW17765) from a malathion susceptible strain of Lucilia cuprina. Comparison with a consensus sequence from derived from clones of the Lc-alpha-E7 resistant allele (see also AAW17768) indicated only one replacement site difference, a Trp to Leu substitution at amino acid position 251 (nucleotide position 752). This mutation is an excellent candidate for the malathion resistance mutation. The
                                     Sequence
                                                                                                                                                                                                                   DNA encoding enzyme that degrades organophosphate pesticides:-useful for decontamination of soil, water, food etc
                                                                                                                                                                                                                                                         P-PSDB;
                                                                                                                                                                                                                                                                    WPI;
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                                                            dimethyl general organophosphates
                                                                                 acid position 251 (nucleotide position 752). This mutation is an excellent candidate for the malathion resistance mutation. The resistant enzyme acts as a malathion carboxylesterase and can be
                                                                                                                                                                                             Claim 4; Fig 1; 52pp; English
                                                                                                                                                                                                                                                                                          Newcomb RD,
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                                                                                                                                                                                                                                                                                                                             (CSIR ) COMMONWEALTH SCI & IND RES ORG
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                                                                        tormulated
                                                                                                                                                                                                                                                       1997-298113/27
DB; AAW17765.
                                     1713 BP;
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D, Oakeshott
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remediation; bioremediation; decontamination;
                                                                        for use in degrading environmental carboxylester
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                                    516 A; 305 C; 370 G; 522 T; 0 other;
 99.3%;
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JG, Robin GC,
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 Score 1701.8;
Pred. No. 0;
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Russell RJ,
           DB 18; Length 1713;
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insecticide; pesticide; water
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    13-JAN-1994;
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                                                                                                                    WO9519440-A1
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water, meat etc.
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|TCGATGTTTGAAAAACATAGAGATTTATTTTAG
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                                                                                                                                                                                                                                                                                                       Pure E3 esterase fi
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pesticide; water decontamination;
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                                          resistant strain, sequenced (Lc7L103 esterases. The es in bioremediation.
                                                          RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding op-susceptible esterase E3 of L. cuprina) from a diazinon resistant strain, Llandillo 103. 4 Isolated clones were sequenced (Lc7L103 A-D, AAQ91562-65) that encoded diazinin resistant esterases. The esterases, or cells expressing them, are used in his resistant transfer.
                                                                                                                                                                                               Example 4; Page 12-17;
                                                                                                                                                                                                                                          water, meat etc.
                                                                                                                                                                                                                                                            Pure E3 esterase from eliminate residues of
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Parker AG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1713 BP; 513 A; 308 C; 368 G; 524 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 4; Page 12-17; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pure E3 esterase from Lucilia cuprina and related DNA - used to eliminate residues of organo:phosphate and carbamate pesticides {\sf C}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              bioremediation.
GCTGCCTCTACCCACTACATGATGTTAACCGAACAAACTCGCGGTCTTTTCCATCGTGGT
                                 AATTGCGCCAACTTTGGTGGCAATCCCGATAATATTACAGTCTTTGGTGAAAGTGCCGGT
                                                               AATTGCGCCAACTTTGGTGGCAATCCCGATAATATTACAGTCTTTGGTGAAAGTGCCGGT .660
                                                                                                                      ATTAACATACAATATCGTTTGGGAGCTCTAGGTTTTCTAAGTTTAAATTCAGAAGACCTT
                                                                                                                                                     GGTGAAAATCATCGTGCTATGTATGGTCCTGATTATTTCATTAAAAAGGATGTGGTGTTG
                                                                                                                                                                 GGTGAAAATCATCGTGATATGTATGGTCCTGATTATTTCATTAAAAAGGATGTGGTGTTG
                                                                                                                                                                                               ATTAACATACAATATCGTTTTGGGAGCTCTAGGTTTTCTAAAGTTTAAATTCAGAAGACCTT
                                                                                                                                                                                                                                        CCCTGGGATGGTGTGCGGGATTGTTGCAATCATAAAGATAAGTCAGTGCAAGTTGATTTT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Campbell PM, Newcomb RD, Oakeshott Robin GC, Russell RJ, Smyth K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94AU-0003347.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97.9%; Score 1676.2;
98.7%; Pred. No. 0;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 16; Length 1713;
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GTGATGAATTGAAAATGATTGATGTGCCTGAAATGGATAAGATTAAACAATGGGAG 1680 	21 ATTA      21 ATTA	Оу 16 рь 16	
SGAAAATGTTTCCTGGGATCCAATTAAGAAATCCGATGAAGTATACAAGTGTTTGAAT 1620 	61 ATC		
ATGGATACAATTTGC            ATGGATACAATTTGC	01 AC9		
AATTGGCCAAACGTATGCCTAAAGAATCGCGTGAATACAAAACAATTGAACGTATG 1500		1 1	
CGTGGTGTTAA(             CGTGGTGTTAA(	181 CGT		
TRACTTGTATCGCTTCGACTTCGATTCGGAAGATCTTATCAATCCCTATCGTATTATG 1380	21 GT	р р	
GGTTCCCCATGCATCGTTTGTTGCAATTACGTTTCAATCACACCTCCGGTACACCC 1320		<u> </u>	
TACAGGAGAACACCAACAGCTGATAAT"	2 C2 C3	, , ,	
ATGCTGAACGCACCGC                 ATGCTGAACGCACCGC	41 0		
ATGCCTATGCTTGTTAAGGAATTGGAAACTTGTGTCAATTTTTGTGCCAAGTGAATTG 1140 	- E	, 1	
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ATTGTGTCTTACCCAAACATCCTCGGGAAATGG' 	61 GC	Db Qy	
AGCGTACAAATAAGGTO	01 0	Ωb	
TTATGAAAGCCAAGCCACAGGATTTAATAAAAC 	41 T3	Qy Db	
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ACTAATGTCGGGTAATGCTATTTGTCCATTGGCTAATACCCAATGTCAACATCGTGCC 780 	721 AT	Qу	
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Best Local Sim
Matches 1689;
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                                                                                                                                                                                                                                                                             Pure E3 es
eliminate
                                                                                                                                                                                                  in bioremediation.
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     CCCTGGGATGGTGTGCGCGATTGTTGCAATCATAAAGATAAGTCAGTGCAAGTTGATTTT
                             ATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCACCCCAGCGACCAACA
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Robin GC,
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                                                                                                                                                      Conservative
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pesticide; water decontamination; meat decontamination;
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98.6%;
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                                                                                                           GCTGATGCTGAACGCACCGCCCCAGAGACCTTGGAAATGGGTGCTAAAATTAAAAAGGCT
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                        GTCTACTTGTATCGCTTCGACTTCGATTCGGAAGATCTTATCAATCCCTATCGTATTATG
                                                                             CATGTTACAGGAGAAACACCAACCGCCGATAATTTTATGGATCTTTGCTCTCACATCTAT
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                GTCTACTTGTATCGCTTCGACTTCGATTCGGAAGATCTTATTAATCCCTATCGTATTATG
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RESULT 8
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A 1710 bp DNA molecule (AAT68597) comprises the Md-alpha-E7 coding sequence of the Musca domestica Rutgers strain. It was isolated by amplification of genomic DNA using alpha-esterase consensus primers (see also AAT68598-99) and use of a 534 bp amplicon to screen a genomic library of M. domestica. A mutation of the gene, resulting in substn. of serine for trypt at amino acid position 251 (see also AAW17767), confers malati
                                                                                                                                                                                                                                                                                                                                                                                                       AAT68597 standard;
                                                                     Claim
                                                                                               DNA
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                                                                                                                                                                                                                                                                                  mutation
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                                                                                      encoding enzyme that degrades organophosphate ful for decontamination of soil, water, food et
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DB; AAW17767.
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"Trp-251 TGG codon is altered
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  23-MAR-2000;
11-JUL-2000;
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                                                                  23-MAR-2001;
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2000US-0614150
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Similarity

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Query Match
Best Local
                                                                            sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).

(ABB57737-ABB72072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent: useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                                                 Claim 1;
                                                                                                                                                                                                                                                                              New isolated nucleic a genes from Drosophila interactions -
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Score 680.4; DB 23; Pred. No. 6.9e-177; 0; Mismatches 636;
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                     AATGTGCCCGGTAATGCCGGCCTTAAAGATCAAGTCATGGCCTTGCGTTGGATTAAAAAT
                                                                                                                                                                GGTGAAAATCATCGTGATATGTATGGTCCTGATTATTTCATTAAAAAGGATGTGGTGTTG
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AATGTACCAGGAAATGCTGGCCTCAAGGATCAGGTGCTGGCCCTCAAGTGGATCAAGAAC
                                                                      GTCACGATACAGTACCGACTTGGGGCTTTGGGATTTATGAGTCTTAAGTCCCCCGAGCTA
                                                                                          ATTAACATACAATATCGTTTGGGAGCTCTAGGTTTTCTAAATTTCAGAAGACCTT
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                                                                                                                                                                                                                                                                                                                                                                        capable of detecting 1000 or more genes from Drosophila. The inventueseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL7737-ABL7072).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genes from Drosophila
interactions -
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genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                      ACTGTGTACGATGATICCTACTACAGTTTTGAGGGTATACCGTACGCCCAACCGCCAGTG 204
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               GACTTCGATTCGGAAGATCTTATCAATCCCTATCGTATTATGCGTAGTGGACGTGGTGTT
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                                                                                                                            genes from Drosophila interactions -
                                                                                                          Claim 1;
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11-JUL-2000;
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL1816176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).

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The sequence data for this patent did not form specification, but was obtained in electronic at ftp.wipo.int/pub/published\_pct\_sequences.

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             CACAGGATTTAATAAAACTTGAGGAAAAAGTTTTAACTCTAGAAGAGCGTACAAATAAGG
                                          TTGGCTACAAGGGCGAGGACAACGACAAGGATGTGCTGGAGTTCTTGCAGAACGTAAAGG
                                                           CCGGCTATAAGGGTGAGGATAATGATAAGGATTTTTTGGAATTTTCTTATGAAAGCCAAGC
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                                                                                                                                                           TGCTAACCGATCAGACCCAAGGGCTCTTTCATCGCGGCATCTTGCAGTCGGGCAGTGCCA
                                                                                                                                                                           TGTTAACCGAACAAACTCGCGGTCTTTTCCATCGTGGTATACTAATGTCGGGTAATGCTA 742
                                                                                                                                                                                                                                   ATCCCGATAATATTACAGTCTTTGGTGAAAGTGCCGGTGCTGCCTCTACCCACTACATGA 682
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Pred. No. 8e-92;
Pred. No. 8e-92;
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RESULT 12
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ABL02099 standard;

cDNA;

1665

ABL02099;

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	703 ATTTATTTT 171	ц
ACAAAG 4973	914	ob 4:
CATAGAG 1702	1643 TTGATGTGCCTGAAATGGATAAGATTAAACAATGGGAGTCGATGTTTGAAAAACATAGAG	2y 1ε
AAGTTCA 4913	854	4
AAAATGA 1642	583 C	2γ 1:
TITION 4853	4794 CTGCCACGGGTAATCCCTACAGCGAGAGATCAACGGTATGACACTCTGACCATTGATC	)b 4:
rGGGATC 1582	523	2γ 1:
CAGTTTG 4793	4734 CGAAGGAAAGTCGCGAGTACAGGAACATCGAACGAACCGTGGGCATCTGGACCCAGTTTG	Ob 4:
CAATTTG 1522	463	Σу 1,
CGGTTGC 4733	4674 GGGTCAGCCATGCCGACGATTTGAGCTACCAATTCAGCAGCCTGCTGGCTCGCCGGTTGC	)b 46
CGTATGC 1462	403 G	2y 1ι
TCAAGG 4673	4614 TCGACTCCGAGGAGCTCATTTTTCCGTACCGCATTATGCGGTTGGGACGCGGTGTCAAGG	)b 40
STTAAGG 1402	343	2γ 1:
rATGACT 4613	554	)b 4:
TTCGACT 1342	283 TG	2γ 1:
CTGAGGG 4553	494 AAGCTGGT	)b 4.
CATCGTT 1282	243	2γ 1:
ATAATCAT 4493	434 AAGCACCCCAGATAATTACATGGATGTAAGTGTCGTCCAATTAGGTGCTTAC	)b 4.
1242	218	Σу 1:
SCTCAGA 4433	4374 TAAAGAAAAACTGGATTCGTGGAGTGCACAGATTCGAGATGTTCATCGCACTGGCTCAGA	Эb 4:
SAGAAAC 1217	1158 CGCCCCAGAGACCTTGGAAATGGGTGCTAAAATTAAAAAGGCTCATGTTACAGG	2у 13
AGCCCAG 4373	4314 GCAGCAGCTTGATGCTGGCACACCTTTCATTCCCAAAGAATTGCTGGCCACGGAGCCC	)b 4:
AACGCAC 1157	098 TAAGGAATTGGAAACTTGT	2γ 10
AGGTGCT 4313	4254 TTCTTTCAATAAGTAAATTTAATTTTATTTCACAGAGGTAAAGCTTATGCCGCAGGTGC	b 4:
rGCTTGT 1097	059	2у 10
TTGAATT 4253		)b 41
1058	040	Σу 10
ATAGGAA 4193	1134 AGCCTCCAAAGGAGATGATGAAGACCGCCTGGAGTAACTCCATCCCCATGTTTATAGGAA	)b 4:1
ATGGGTA 1039	980 AACATCCTCGGGAAATGGTTAAAACTGCTTGGGGTAATTCGATACCCACTATGA	Σy
TATCCA 4133	YZO TCATISTITICCITYTIGGTCCCACTGITENGCCALATCHGACCGCCGAATGTGTGATATCCACTGAACCATTCCCACGCCCGAATGTGTGATATCCACCACTGCAACCATTCCTCCACGCCCGAATGTGTGATATCCA	25 4c
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                                                                                                                                                                                                                                                                                                                                                    capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukarytes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid genes from Drosophila and interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster.
                                                                                                                                                                                                                                                                                          Sequence 1665 BP;
                                                                                                                                                                                                                                                                                                                        The sequence data for this patent did not form part of the prispecification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                    The
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 779; 21pp + Sequence Listing; English.
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pharmaceutical;
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                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                      invention relates to an isolated nucleic acid detection reagent able of detecting 1000 or more genes from Drosophila. The invent
CAAAGAATTTGTATCCCACCAAACCAATGCCCGTGATGGTCTGGATCTATGGCGGTGGCT
                                                                                                                                                                CCTACGGACCCATCAAGGGTGTAAAGAGGAAGTCCATCTACGGCCAGTCCTACTTCAGCT
                                                                                                                                                                                                                             TTGAAAATAAGTTTTTAAACTATCGTTTAACTACCAATGAAACGGTGGTAGCTGAAACTG 112
              CCCCGGAGGTCTGGAGGTCAGGAGCTGCACCTCCCAGGGTCCCAAGCCACTGCAGA
                                                                                                    GACCAACACCCTGGGATGGTGCGCGATTGTTGCAATCATAAAGATAAGTCAGTGCAAG
                                                                                                                         TCGAGCGGATCCCCTTCGCCAAACCACCGGTGGGCGAGCTACGCTACAAGGCTCCCCAGC
                                                                                                                                              TTGAGGGTATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCACCCCAGC
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)B; ABB57996.
                                                            TTGATTTTATAACGGGCAAAGTGTGTGGCTCAGAGGATTGTCTATACCTAAGTGTCTATA
                                                                                                                                                                                                         TCGACTTTAAGGTCCAACAACGACGATACAGGACCAGCGAAAAGACTGTCGTCAGCACCA
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2000US-0614150
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CAATTGAACGTATGACTGGTATATGGATACAATTTGCCCACCACTGGTAATCCTTATAGCA
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                                                                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticedes, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                 Sequence
                                                                                                                                                                                            Claim 1; SEQ ID NO 8549; 21pp + Sequence Listing; English
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                                                                                 he sequence data for this patent did not form part of the printed pecification, but was obtained in electronic format directly from it ftp.wipo.int/pub/published_pct_sequences.
                           Local Similarity
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TTGAAAATAAGTTTTTAAACTATCGTTTAACTACCAATGAAACGGTGGTAGCTGAAACTG
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention
                                                                            New isolated nucleic acid genes from Drosophila and interactions -
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 TCTCAGCAACGATGAAAAGCATCATCGGATCCTTTTCGCCTTCGGACCTGTCGTAGAACC
                  TTTAACTCTAGAAGAGCGTACAAATAAGGTCATGTTTCCTTTTGGTCCCACTGTTGAGCC
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                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic a genes from Drosophila interactions -
                                                                                                                                      The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                  Sequence 1863 BP; 425 A; 493 C;
                                                                                                                         at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO
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CTGGTGGGCATGTGGCATTCGCCCGAAACGACAATCCCAATTG 1709
               ATGACTGGTATATGGATACAATTTGCCACCACTGGTAATCCTTATAG 1544
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                                                                                                         GTGATGTGCGGAAAACACGTTCGCGGAGTTAGTCATGCCGACGATCTCTCCTACCTTTTC 1602
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Search completed: April 11, 2003, 01:06:03 Job time: 263.905 secs

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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Reoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 778)
HarveyD., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang
Lewis, S. and Rubin, G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                                                                                  A1062034 778 bp mRNA linear EST 19-APR-2001 GH01076.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH01076 5prime similar to U51050: Drosophila melanogaster alpha esterase (aE7) gene, partial cds,
                                                                 Lawrence Berkeley
One Cyclotron Rd,
Fax: 510 486 6798
                                Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: 10 row: G column: 4
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quality sequence stop: 363.
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AI388926 649 bp mRNA linear EST 19-APR-GH19977.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH19977 5prime similar to U51050: Drosophila melanogaster alpha esterase (aE7) gene, partial Cds.
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82 a 196 c 220 g 180 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                431 ATCGTGATATGTATGGTCCTGATTATTTCATTAAAAGGATGTGGTGTTGATTAACATAC 490
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                                                                                                                                                                                                                                                                                                                                                                                                                              4 ATCGGGAATGGTATGGCCCGGATTACTTTATGAAAGAAGATGTTGTTCTCGTCACGATAC
                                                                                                                                                                                                                                                                                                         mRNA sequence.
AI388926
AI388926.1 GI
                                                                                                                                                                                                     CCCACTACATGATGTTAACCGAACAAACTCGGGGTCTTTTCCATCGTGGTATACTAATGT 730
                                                                                                                                                                                                                                                                  ACTTTGGTGGCAATCCCGATAATATTACAGTCTTTTGGTGAAAGTGCCGGTGCTGCTCTA 670
                                                                                                                                                                                                                                                                                                                                                                     AGTACCGACTTGGGGCTTTGGGATTTATGAGTCTTAAGTCCCCCGAGCTAAATGTACCAG 123
                                                                                                                                       CGGGTAATGCTATTGTCCATTGGCTAATACCC---AATGTCAACATCGTGCCTTCACCT
                                                                                                                                                                                     AGAACGTAAAGGCCAAGGATCTTATTCGCGTGGAGGAAAATGTCCTGACACTGGAGGAAC
                TGAAAGCCAAGCCACAGGATTTAATAAAACTTGAGGAAAAAGTTTTAACTCTAGAAGAGC
                                                         TAGCCAAGCTGGTTGGCTACAAGGGCGAGGACAACGACAAGGATGTGCTGGAGTTCTTGC
                                                                           TAGCCAAATTGGCCGGCTATAAGGGTGAGGAGATAATGATAAGGATGTTTTGGAATTTCTTA
                                                                                                                        Email: http://www.fruitfly.org/EST, plate: 199 row: G column: 5
High quality sequence stop: 559.
Location/Qualifiers
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Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
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Neoptera; Endopterygota; Diptera; Brachycera; Musco
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 649)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="GH19977"
/clone=lib="GH Drosophila melanogaster head pOT2" /
/sex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
/note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
/note="Organ: head; Vector: pOT2; Sized fractionated cDNAs were directly ligated into
xho1; Sized fractionated cDNAs were directly ligated into
poT2. Plasmid cDNA library."

pOT2. Plasmid cDNA library."
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Berkeley, CA
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                                                     AAAGTGAAAGGCGTTAAACGTTTAACTGTGTACGATTGCTACTACTACTATTTTGAGGGT 180
                                                                                                                       AAGTTTTTAAACTATCGTTTAACTACCAATGAAACGGTGGTAGCTGAAACTGAATATGGC 120
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ATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCACCCCAGCGACCAACA
                                                                                                                                                                                                           ATGAATTTCAACGTTAGTTTGATGGAGAATTAAAATGGAAGATTAAATGCATTGAAAAT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGTTTATAGGAAACACTTCGTACGAGGGCCTGCTGT 639
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                                CAAGTGAGGGGTATCAAGCGTCTATCTCTCTACGATGTGCCCTACTTCAGCTTCGAGGGT
                                                                                                    AAAGTCCAGCAGTATCGCCAGTCGACCAATGAAACAGTTGTCGCCGACACGGAGTACGGC
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                                                                                                                                                                                                                                                 391;
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Drosophila melanogaster alpha esterase (aE7) gene, partial cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lewis, S. and Rubin, G.M. BDGP/HHMI Drosophila EST Project Unpublished (2001)
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Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophillade; Drosophila.
1 (bases 1 to 688)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: http://www.fruitfly.org/EST, Plate: 230 row: C column: 12
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One Cyclotron Rd, Berkeley, CA 94720,
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                                                                                                                                                                                                                                                                                                                                /clone_lib="GH Drosophila melanogaster/sex="male and female"
/sex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
/note="Organ: head; Vector: pOT2; Site
XhoI; Sized fractionated cDNAs were di
pOT2. Plasmid cDNA library."
la 174 c 197 g 156 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
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Pred. No. 5.7e-62;
0; Mismatches 207
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NAs were directly ligated into
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A1517692 671 bp mRNA linear EST 19-APR GH28740.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster similar to U51050: Drosophila melanogaster alpha esterase (aE7) gene, partial cds
                                                                                                                                                                                                                                                                                                                                                                    Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
                                                                                                                                                                                                                                Email: http://www.fruitfly.org/EST, Plate: 287 row: D column: 4 High quality sequence stop: 538.
                                                                                                                                                                                                                                                                                     One Cyclotron Rd, Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST
                                                                                                                                                                                                                                                                                                                                                      Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                                                                                                       Harvey,D., Brokstein,P., Hong,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Ephydroidea; Drosophilidae; Drosophila
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                 155
        рот2.
170
          /clone_lib="GH Drosophila melanogaster head
/sex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
/note="Organ: head; Vector: pOT2; Site_1: Ec
xho1; Sized fractionated cDNAs were directly
pOT2. plasmid cDNA library."
a 170 c 193 g 153 t
                                                                                                                                                                 /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
                                                                                                                                                     /clone="GH28740"
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                                                                                                                                                                                                                                                                     est@fruitfly.berkeley.edu
                                               pOT2; Site_1: EcoRI; Site_2:
NAs were directly ligated into
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Query Match Best Local Similarity

15.1%;

Score Pred.

258.2; DB 9 No. 1.3e-59;

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Length

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REFERENCE
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                         Lawrence Berkeley
One Cyclotron Rd,
Fax: 510 486 6798
                                                                                                                                                    I (bases 1 to 569)

Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, Li, P., Liao, G., Misra, S., R., Gonzalez, M., Guarin, H., Harrits, N., Li, P., Liao, G., Misra, S., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and Rubin
                                                                                                                BDGP/HHMI RH Drosophila Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                              B1609541 Sprime RH Drosophila melanogaster normalized Head pFIc-1 Drosophila melanogaster clone RH14337 Saimilar to alpha-Est7: FBan0001112 GO:[carboxyesterase (GO:0004091); carboxyesterase (GO:0004091)] located on: 3R 84D5-84D5;: 08/17/2001, mRNA sequence.
                                                                                                                                                                                                                                                             Eukaryota; Metazoá; Arthropoda; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Muscc
Ephydroidea; Drosophilidae; Drosophila.
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     http://www.fruitfly.org/EST, est@fruitfly.berkeley
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              BI628316 674 bp mRNA linear EST 10-SEP-2001 RH56682.5prime RH Drosophila melanogaster normalized Head pFlc-1 Drosophila melanogaster cDNA clone RH56682 5 similar to alpha-Est7: FBan0001112 GO:[carboxyesterase (GO:0004091); carboxyesterase (GO:0004091)] located on: 3R 84D5-84D5;: 08/22/2001, mRNA sequence.
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/dev_stage="Adult"
/lab_host="DH5-alpha TonA"
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/db_xref="taxon:7227"
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Pred. No. 4.8e-59;
0; Mismatches 195;
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   GGTGAAAATCATCGTGATATGTATGGTCCTGATTATTTCATTAAAAAGGATGTGGTGTTG
                                                               GTGAAGCCCGACAAGGCTCGCCCGGTTATGGTTTGGATTCACGGAGGAGGCTTCATTATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: 510 486 6798
Email: http://www.fruitfly.org/EST,
Plate: RH.566 row: G column: 10
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One Cyclotron Rd, Berkeley, CA 94720, USA
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pFIc-1"
/sex="male and female"
/sex="male and female"
/dev_stage="Adult"
/lab_host="DHS-alpha TonA"
/lab_host="DHS-alpha TonA"
/note="Organ: head, vector: pFIc1; Site_1: XhoI; Site_2:
/note="organ: head, vector: pFIc1; Site_1: XhoI; Site_2:
BamHI; Library was kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using 're recombinase. Plasmid cDNA library."

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/db_xref="taxon:7227"
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ATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCACCCCAGCGACCAACA
                                                                                                                                     AAGTTTTTAAACTATCGTTTAACTACCAATGAAACGGTGGTAGCTGAAACTGAATATGGC
                                                                                                                                                                                   ATGAATAAGAACCTCGGCTTTGTGGAGCGCCTTGCGGTGGCGCCTCAAAACCATCGAGCAT
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                                                                                 AAAGTGAAAGGCGTTAAACGTTTAACTGTGTACGATGATTCCTACTACAGTTTTGAGGGT
                                                                                                                   AAAGTCCAGCAGTATCGCCAGTCGACCAATGAAACAGTTGTCGCCGACACGGAGTACGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lawrence Berkeley
One Cyclotron Rd,
Fax: 510 486 6798
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Neoptera; Endopterygota; Diptera; Brachycera;
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quality sequence stop: 641.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                               /note="vector: por2; Site_1: fractionated cDNAs were directly plasmid cDNA library." 154 t 173 c 194 g 154 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="SD16705"
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Pred. No. 1.2e-57;
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directly ligated into pOT:
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                                                                                                                                                                                                                                                                                Length 676;
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673 bp mRNA linear EST 07-SEP-2001
RH43493.5prime RH Drosophila melanogaster normalized Head pFlc-1
Drosophila melanogaster cDNA clone RH43493 5 similar to alpha-Est7:
FBan0001112 GO:[carboxyesterase (GO:0004091); carboxyesterase
(GO:0004091)] located on: 3R 84D5-84D5;: 08/18/2001, mRNA sequence.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Muscc
Ephydroidea; Drosophilidae; Drosophila.
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BI614181.1 GI:15509706
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Email: http://www.fruitfly.org/EST,
plate: RH.434 row: H column: 9
High quality sequence stop: 553.
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One Cyclotron Rd, Berkeley, CA 94720,
Fax: 510 486 6798
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                                                                                                                        /clone_lib="RH Drosophila melanogaster normalized
pFlc-1"
                                                                                                                                                         /organism-"Drosophila
/db_xref-"taxon:7227"
/clone-"RH43493"
/note-"Organ: head; Vector: pFlc1; Site_1: XhoI; Site_2: BamHI; Library was kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library."
                                                                   /sex="male and female"
/dev_stage="Adult"
/lab_host="DH5-alpha TonA"
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Muscomorpha;
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                                                                                    Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Inst
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                   carboxyesterase, mRNA sequence.
                                                                                                                                                                            в1639486.1
                                           BDGP/HHMI Drosophila EST
Unpublished (2001)
                                                                 Harvey,D., Brokstein,P., Hong,L., Lewis,S. and Rubin,G.M.
Lawrence Berkeley National One Cyclotron Rd, Berkeley,
                                Contact: Stapleton,
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RH43812.5prime RH Drosophila melanogaster normalized Head pFlc-1
Drosophila melanogaster cDNA clone RH43812 5 similar to alpha-Est7:
FBan0001112 GO:[carboxyesterase (GO:0004091); carboxyesterase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High
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Plate: SD.220 row: F column: 7
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/clone_lib="SD Drosophila melanogaster Schneider L2
culture pOT2"
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170 c 176 g 145 t
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/db_xref="taxon:7227"
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                                                    GTCTTCGATAAGGTAGAGGGCTCCGAGGACTGCCTCTATCTCAATGTGTACACCAACAAT
                                                                      ATAACGGGCAAAGTGTGTGTGTGAGAGGATTGTCTATACCTAAGTGTCTATACGAATAAT
                                                                                                                                                                                                                              ATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCACCCCAGCGACCAACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: http://www.fruitfly.org/EST, Plate: RH.438 row: A column: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2001) Contact: Stapleton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BDGP/HHMI RH Drosophila EST Project
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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BI614443.1 GI:15509968
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/db_xref="taxon:7227"
/clone="RH43812"
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                         61
                                                                                                                                                                     Local Similarity
                                                                                    1 ATGAATTTCAACGTTAGTTTGATGGAGGAAATTAAAATGGAAGATTAAATGCATTGAAAAT 60
AAGTTTTTAAACTATCGTTTAACTACCAATGAAACGGTGGTAGCTGAAACTGAATATGGC 120
                                                             ATGAATAAGAACCTCGGCTTTGTGGAGCGCCTTGCGGTGGCGCCTCAAAACCATCGAGCAT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTAACATACAATATCGTTTGGGAGCTCTAGGTTTTCTAAGTTTAAATTCAGAAGACCTT
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Email:
Plate:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 670)
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RROPA 1 inear EST 11-JUL-2001

RRC29491 5prime RE Drosophila melanogaster normalized Embryo pFlc-1

Drosophila melanogaster cDNA clone RE29491 5 similar to alpha-Est7:

FBan0001112 located on: 3R 84D5-84D5;: 04/12/2001, mRNA sequence.

BI233202

BI233202.1 GI:14700784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ,R., Gonzalez,M., Guarin,H., Harris,N., Li,P., Liao,G., Misra,S., Mungall,C.J., Nunoo,J., Pacleb,J., Paragas,V., Park,S., Phouanenavong,S., Wan,K., Yu,C., Lewis,S.E., Celniker,S. and Rubin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., C., J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fruit fly.
                                                                                                                                                                                                                                                     152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1: http://www.fruitfly.org/EST, e: RE.294 row: H column: 7 quality sequence stop: 534.
                                                                                                                                             Conservative
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                                                                                                                                                                                                                                             /dev_male and female"
/dev_stage="0-24 hours mixed stage embryonic"
/lab_host="DH5-alpha TonA"
/note="Organ: embryo; Vector: pFlc1; Site_1: XhoI; Sit
BamHI; Library was kindly generated by Piero Carninci
the RIKEN. The library was normalized and excised usi
Cre recombinase. Plasmid cONA library."
168 c 194 g 155 t l others
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="RE29491"
                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="RE Drosophila melanogaster normalized
prlc-1"
                                                                                                                                                                   14.5%;
65.1%;
                                                                                                                                                0;
                                                                                                                                           Score 248; DB 13;
Pred. No. 7.9e-57;
0; Mismatches 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  est@fruitfly.berkeley.edu
                                                                                                                                             196;
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                    One Cyclotron Rd, Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA
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Drosophila
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                                                           /sex="male and female"
/dev_stage="adult"
                                                                                                                          /clone="GH10213"
/clone_lib="GH Drosophila
                                                                                                                                                                                             /organism="Drosophila
/db_xref="taxon:7227"
                                    /lab_host="DH5 -
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Vector:

porz;

Site\_1:

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Site\_2:

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                                      Harvey,D., Brokstein,P., Hong,L.,
Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
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Drosophila melanogaster alpha esterase (aE7) gene, partial cds.
               BDGP
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Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
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Lawrence Berkeley National Lab
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AI109901
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GH09292.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH09292 5prime similar to U51050:
Drosophila melanogaster alpha esterase (aE7) gene, partial cds, mRNA sequence.
AI109901
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/dev_stage="adult"
/lab_host="DH5 - alpha"
/note="Organ: head; Vector: pOT2; Site_1: Ec XhoI; Sized fractionated cDNAs were directly pOT2. Plasmid cDNA library."
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Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
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1 (bases 1 to 646)
                                                                                                                 GTCTTCGATAAGGTAGAGGGCTCCGAGGACTGCCTCTATCTCAATGTGTACACCAACAAT
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ATTAACATACAATATCGTTTGGGAGCTCTAGGTTTTCTAAGTTTAAATTCAGAAGACCTT 540
                                            One Cyclotron Rd,
Fax: 510 486 6798
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plate: 92 row: H column: 8
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One Cyclotron Rd, Berkeley, CA 94720, USA
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/db_xref="taxon:7227"
/clone="6H09292"
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/dev_stage="adult"
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/lab_host-"DH5 - alpha"
/note-"Organ: head; Vector: pOT2; Site_1: EcoRI; Site
/note-"Organ: head; Vector: pOT2; Site_1: EcoRI; Site
/note-"Organ: head; Vector: pOT2; Sized fractionated cDNAs were directly ligated
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Pred. No. 5.2e-56;
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Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
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Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 646)
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High quality sequence stop: 493.
Location/Qualifiers
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Fax: 510 486 6798
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Site_2: Xhol; Sized fractionated cDNAs w
ligated into POT2. Plasmid cDNA library.
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/db_xref="taxon:7227"
/clone="LP06524"
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/dev_stage="larvae-pupae"
/lab_host="DH5-alpha"
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Pred. No. 5.2e-56;
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3: /cgn2_6/ptodata/1,
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# ALIGNMENTS

US/09068960A

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GENERAL INFORMATION:
APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org.
TITLE OF INVENTION: MALATHION CARBOXYLESTERASE
FILE REFERENCE: Attorney Docket No. 6235515 50179-051
CURRENT APPLICATION NUMBER: US/09/068,960A
CURRENT FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER APPLICATION NUMBER: AU 6751
EARLIER FILING DATE: 1996-11-23
EARLIER FILING DATE: 1995-11-23
NUMBER OF SEQ ID NOS: 43
SOFTWARE PATENTIN Ver. 2.0
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; TYPE: DNA; ORGANISM: Lucilia cuprina US-09-068-960-3
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Sequence 9, Application US/09068960A

Patent No. 6235515
GENERAL INFORMATION:
APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org
TITLE OF INVENTION: MALATHION CARBOXYLESTERASE
FILE REFERENCE: Attorney Docket No. 6235515 50179-051
CURRENT APPLICATION NUMBER: US/09/068,960A
CURRENT FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER FILING DATE: 1996-11-23
NUMBER OF SEQ ID NOS: 43
NUMBER OF SEQ ID NOS: 43
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; SOFTWARE: PATENTIN V
; SEQ ID NO 9
; LENGTH: 1713
; TYPE: DNA
; ORGANISM: Lucilia c
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APPLICANT: Commonwealth Scientific and Industrial Rsr
TITLE OF INVENTION: MALATHION CARBOXYLESTERASE
FILE REFERENCE: Attorney Docket No. 6235515 50179-051
CURRENT APPLICATION NUMBER: US/09/068,980A
CURRENT FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EEARLIER FILING DATE: 1996-11-22
EARLIER FILING DATE: 1995-11-23
INUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1
LENGTH 113
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APPLICANT: COMMONWEALTH Scientific and Industrial Rsrch.
APPLICANT: COMMONWEALTHION CARBOXYLESTBRASE
TITLE OF INVENTION: MALATHION CARBOXYLESTBRASE
FILE REFERENCE: Attorney Docket No. 623515 50179-051
CURRENT APPLICATION NUMBER: US/09/068,960A
CURRENT FILLNG DATE: 1998-05-20
CURRENT FILLNG DATE: 1998-05-20
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER FILLNG DATE: 1995-11-22
EARLIER FILLNG DATE: 1995-11-23
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patcentin Ver. 2.0
SEQ ID NO 5
LENGTH: 1713
TYPE: DNA
ORGANISM: Lecilia cuprina
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Conservative
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Pred. No. 0;
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US-08-669-524-1
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Matches 1706
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1713 base pairs
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APPLICANT:
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REFERENCE/DOCKET NUMBER: 14
TELECOMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEPAX: 703-684-1124
                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY_AGENT INFORMATION:
NAME: Price, Robert L.
NAME: Price, Robert L.
22,685
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,524
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MEDIUM TYPE: Floppy disk
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COUNTRY: USA
ZIP: 22314
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CITY: Alexandria
STATE: Virginia
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BOYCE, Thomas M.
CAMPELL, Peter M.
PARKER, Anthony G.
OAKESHOTT, John G.
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                   GCTGATGCTGAACGCACCGCCCCAGAGACCTTGGAAATGGGTGCTAAAATTAAAAAGGCT
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                                                           GCTGATTGTGTCTTACCCAAACATCCTCGGGAAATGGTTAAAACTGCTTGGGGGTAATTCG
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Sequence 7, Application:
Sequence 7, Application:
Patent No. 6235515
GENERAL INFORMATION:
APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org
ITILE OF INVENTION: MALATHION CARROXYLESTERASE
FILE REFERENCE: Attorney Docket No. 6235515 50179-051
CURRENT APPLICATION NUMBER: US/09/068,960A
CURRENT FILING DATE: 198-05-20
CURRENT FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER APPLICATION NUMBER: AU 6751
EARLIER FILING DATE: 1995-11-23
NUMBER OF SEQ ID NO7
SEQ ID NO 7
LENGTH: 1713
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Best Local Similarity 99.6%;
Matches 1706; Conservative
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Pred. No. 0;
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RESULT 7
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                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,524
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Price, Robert L.
REGISTRATION NUMBER: 22,685
REFERENCE/DOCKET NUMBER: 1451-021
RELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1121
TELEPAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: ROBIN, Geoffrey C. APPLICANT: BOYCE, Thomas M. APPLICANT: CAMPELL, Peter M. APPLICANT: PARKER, Anthony G. APPLICANT: OAKESHOTT, John G. APPLICANT: SMYTH, Kerrie A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: OAKESHULL, CARPLICANT: SMYTH, Kerrie A. TITLE OF INVENTION: ENZYME
                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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APPLICANT: NEWCOMB, Richard
APPLICANT: ROBIN, Geoffrey (
APPLICANT: BOYCE, Thomas M.
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                                                                                                                                                                                                                                                                                                                                        STREET: 99 Canal (CITY: Alexandria STATE: Virginia COUNTRY: USA ZIP: 23314
LENGTH: 1713 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
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Best Local Similarity 98.0
Matches 1679; Conservative
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TITLE OF INVENTION: MALATHION CARBOXYLESTERASE
FILE REFERENCE: Attorney Docket No. 6235515 50179
CURRENT APPLICATION NUMBER: US/09/068,960A
CURRENT FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER FILING DATE: 1996-11-22
EARLIER FILING DATE: 1996-11-22
EARLIER FILING DATE: 1995-11-23
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 14
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GENERAL INFORMATION:
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TYPE: DNA
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Pred. No. 3.4e-268;
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                                                                                                                                                                                             Sequence 51, Application US/08747221B Patent No. 6063610 GENERAL INFORMATION:
                                                                                                   APPLICANT: Silver, Gary W.
APPLICANT: Wisnewski, Nancy
TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
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         ADDRESSEE: Carol Talkington Ve.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
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Heska Corporation
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,221B
FILING DATE: NO. 6063610ember 12, 1
CLASSIFICATION: 435

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ATTORNEY/AGENT INFORMATION

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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; NAME/KEY: CDS
; LOCATION: 1..1584
US-08-747-221B-51
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RESULT 10
US-08-747-221B-52/c
US-08-747-221B-52/c
; Sequence 52, Application US/08747221B
; Patent No. 6063610
; Patent INFORMATION:
; GENERAL INFORMATION:
; CANDILICANT: Silver, Gary W.
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NEORMATION FOR SEQ ID NO: 51:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 ATGGCAAAGTGAAAGGCGTTAAACGTTTAACTGTGTACGATGATTCCTACTACAGTTTTG 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 AGGGTATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCACCCCAGCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149 CAGAACCTTGGTCAGGTGTTCTTGATGCTAGTAAAGAAGGGAATAGTTGTAGATCAGTAC 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89 CTGGAATTTCCATATGCCAAACCTCCTGTAGGTGATCTAAGATTTAAGCCACCTCAACCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAAAACATCAGAGAAATCACTTCCTTCCAGTAATGGTATGGATACATGGAGGAGGCTTCT 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAACACCCTGGGATGGTGCGCGATTGTTGCAATCATAAAGATAAGTCAGTGCAAGTTG 295
                                                                                                                                                                                                                                                                                                                                                                           TGTTGATTAACATACAATATCGTTTGGGAGCTCTAGGTTTTCTAAGTTTAAATTCAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                   TCATGGGATCTGGAAATAGTGATATGTATGGTCCTGAATATTTGATGGATTATGGAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                    TTATCGGTGAAAATCATCGTGAFATGTATGGTCCTGATTATTTCATTAAAAAGGATGTGG
                                                                                                                                                                                                                                                                                                                       ACCTTAATGTGCCCGGTAATGCCGGCCTTAAAGATCAAGTCATGGCCTTGCGTTGGATTA 595
                                                                                                                                                                                                                                                                                                                                                            TTCTGGTTACTTTCAATTATCGATTAGGTGTTTTTGGGATTTTTGAACCTGGGAATAGAAG
                                                                                                                                                      GTGGTATACTAATGTCGGGTAATGCTATTTGTCCATTGGC 755
                                                                                                                                                                                                    CCGGTGCTGCCTCTACCCACTACATGATGTTAACCGAACAAACTCGCGGTCTTTTCCATC 715
                                                                                                                                                                                                                                                                                                  AA-----GCGCCTGGCAATGTTGGTTTGATGGACCAGGTTGAAGCTCTAAAATGGGTAA
                                                                                                                           AAGCGATCTCACAAAGTGGAAGTGCTTTTAATCCTTGGGC 662
                                                                                                                                                                                                                                           AAAACAATATTGCATCCTTTGGTGGTGACCCCAACAATGTGACTATTTTTGGAGAATCAG
                                                                                                                                                                                                                                                               AAAATAATTGCGCCAACTTTGGTGGCAATCCCGGATAATATTACAGTCTTTGGTGAAAGTG
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pred. No. 4.9e-42;
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US-08-747-221B-52
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Best Local S
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APPLICATION NUMBER: US/08/74/.22:
FILING DATE: No. 603610ember 12
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
NAME: Verser, Carol Talkington
REFEITRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELECHONE: 970/493-7272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO:
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TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1584 nucleotid
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TOPOLOGY: lir
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1825 Sharp Point Drive CITY: Fort Collins
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                                                                                                                                                                                                                                                                                                         1436
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                                                                                                                                                                                                                                                                                                                                   CAACACCCTGGGATGGTGTGCGCGATTGTTGCAATCATAAAGATAAGTCAGTGCAAGTTG 295
                                                                                                                                                                                                                                                                                                      CAGAACCTTGGTCAGGTGTTCTTGATGCTAGTAAAGAAGGGAATAGTTGTAGATCAGTAC 1377
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                                                                                                                                                                                                                                             ATTTTATTAAAAAAATTAAAGTAGGGGCTGAAGATTGTTTATACCTCAATGTCTATGTAC 1317
                                                                                                                                                                                                                                                                          ATTITATAACGGGCAAAGTGTGTGTGGCTCAGAGGATTGTCTATACCTAAGTGTCTATACGA 355
                                                                                                                                       TTATCGGTGAAAATCATCGTGATATGTATGGTCCTGATTATTTCATTAAAAAGGATGTGG 475
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                                                                                      TGTTGATTAACATACAATATCGTTTGGGAGCTCTAGGTTTTCTAAGTTTAAATTCAGAAG 535
                                                            TTCTGGTTACTTTCAATTATCGATTAGGTGTTTTGGGATTTTTGAACCTGGGAATAGAAG 1137
   AA----
                   ACCTTAATGTGCCCGGTAATGCCGGCCTTAAAGATCAAGTCATGGCCTTGCGTTGGATTA 595
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   -GCGCCTGGCAATGTTGGTTTGATGGACCAGGTTGAAGCTCTAAAATGGGTAA 1083
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No. 6063610ember 12, 1
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pred. No. 4.9e-42;
0; Mismatches 275;
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US-09-005-051-51
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US-09-005-051-51
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Matches 359
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                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
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APPLICANT: Wisnewski,
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                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1584 nucleotid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
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                                   176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Carol Talkington Verser, Ph.D. ADDRESSEE: Heska Corporation STREET: 1825 Sharp Point Drive CITY: Fort Collins
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TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Verser, Carol Talkington REGISTRATION NUMBER: 37,459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                                                                                                                                                                                     NAME/KEY:
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CTGGAATTCCATATGCCAAACCTCCTGTAGGTGATCTAAGATTTAAGCCACCTCAACCTG
                    AGGGTATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCACCCCAGCGAC
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                                                                    AAGGTACTTTAAAAAGGAAAAGAGCAAATTAGTGAAAAAAGGAAATGTGTTCCATAGTTATT
                                                                                                        ATGGCAAAGTGAAAGGCGTTAAACGTTTAACTGTGTACGATGATTCCTACTACAGTTTTG 175
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o. 6291222
                                                                                                                                           il Similarity 56.3
359; Conservative
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Wisnewski, Nancy
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                                                                                                                                                                                                                                                                                                      linear
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                                                                                                                                       Score 178; DB 4; 1
Pred. No. 4.9e-42;
0; Mismatches 275;
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                                                                                                                                                                           Length 1584;
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RESULT 12
US-09-005-051-52/c
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APPLICATION NUMBER: 08/747,221
FILING DATE: NO. 6291222ember 12,
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Silver, Gary W.
APPLICANT: Wisnewski, Nancy
TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
                                                                                                                        FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                        STATE:
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RESULT 13
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                                                                                                                                                 Sequence 36, Application US/08747221B Patent No. 6063610 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 10.4%;
Best Local Similarity 56.1%;
Matches 359; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1584 nucleotide
                                                                    APPLICANT: Silver, Gary W.
APPLICANT: Wisnewski, Nancy
TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
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                                   NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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 ADDRESSEE:
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STRANDEDNESS: single
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Heska Corporation
             Carol Talkington Verser,
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Pred. No. 4.9e-42;
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; LOCATION:
US-08-747-221B-36
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Best Local
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ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 970/484-9505 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA
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                  596 AAAATAATTGCGCCAACTTTGGTGGCAATCCCCGATAATATTACAGTCTTTGGTGAAAGTG
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les 359; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1825 Sharp
CITY: Fort Collins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                        ACCTTAATGTGCCCGGTAATGCCGGCCTTAAAGATCAAGTCATGGCCTTGCGTTGGATTA 595
                                                                                                                                                            TGTTGATTAACATACGATATCGTTTGGGAGCTCTAGGTTTTCTAAGTTTAAATTCAGAAG
                                                                                                                                                                                                                                   TTATCGGTGAAAATCATCGTGATATGTATGGTCCTGATTATTATAAAAAAGGATGTGG 475
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AAAACAATATTGCATCCTTTGGTGGTGACCCCAACAATGTGACTATTTTTGGAGAATCAG
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                                                                    -GCGCCTGGCAATGTTGGTTTGATGGACCAGGTTGAAGCTCTAAAATGGGTAA
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56.1%;
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Pred. No. 5.5e-42;
0; Mismatches 275;
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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LENGTH: 2007 nucleotides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
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                                                                                                              1849
                                                                                                                                                                                                                                                       1969 AAGGTACTTTAAAAGGAAAAGAGCAAATTAGTGAAAAAGGAAATGTGTTCCATAGTTATT 1910
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                                                                                                                                                                                                       176 AGGGTATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCACCCCAGCGAC 235
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NAME: Verser, Carol Talkington REGISTRATION NUMBER: 37,459 REFERENCE/DOCKET NUMBER: FC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: NO. 60 CLASSIFICATION: 43
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TOPOLOGY: linear
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                                                                     ATTTTATAACGGGCAAAGTGTGTGGCTCAGAGGATTGTCTATACCTAAGTGTCTATACGA 355
                                                                                                           CAGAACCTTGGTCAGGTGTTCTTGATGCTAGTAAAGAAGGGAATAGTTGTAGATCAGTAC 1790
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                                     ATTTTATTAAAAAATTAAAGTAGGGGCTGAAGATTGTTTATACCTCAATGTCTATGTAC 1730
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6063610ember 12,
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APPLICANT: Silver, Ga
APPLICANT: Wisnewski,
                                                                                                              TELEFAX: 970/484-9505 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/747,221 FILING DATE: NO. 6291222ember ATTORNEY/AGENT INFORMATION:
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MOLECULE
                                                                                            SEQUENCE CHARACTERISTICS:
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                 TOPOLOGY: li
                                                                                                                                                                                                          NAME: Verser, Carol Talkington REGISTRATION NUMBER: 37,459
                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
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Search completed: April 11, 2003, 08:51:16 Job time : 46.5118 secs
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                                        633 AAGCGATCTCACAAAGTGGAAGTGCTTTTAATCCTTGGGC 672
                                                     716 GTGGTATACTAATGTCGGGTAATGCTATTTGTCCATTGGC 755
                                                                                 573 CAGGTGGTGCAAGTGTTCATTATTTGATGTTATCAGATCTTTCCAAAGGACTTTTTCATA 632
                                                                                             656 CCGGTGCTGCCTCTACCCACTACATGATGTTAACCGAACAAACTCGCGGTCTTTTCCATC 715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              April 11, 2003, 01:07:17; Search time 94.5276 Seconds
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Listing first 45 summaries
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/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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15895.765 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Score	% Query Match	Length	DB	ID	Description
_ :	8.88	5.2	1691	إ و	US-10-083-590-13	Sequence 13, Appl
2	78.8	4.6	1611	9	US-09-738-626-1254	1254
ω		з. 6	1967	10	US-09-748-739A-1	e 1, A
4	62.2	3.6	2381	10	US-09-880-107-2271	
u		ა . ნ	2416	10	US-09-748-739A-3	
6		3.6	2416	10	US-09-748-739A-5	5
7		3.6	2416	10	US-09-748-739A-7	Sequence 7, Appli
80		3.6	2416	10	US-09-748-739A-16	16,
9		3.6	2444	9	US-09-893-519A-112	112,
10		3.4	657	10	US-09-974-300-1107	07
11		3.4	2508	10	US-09-934-323-3	ő
12	57.6	3.4	4667	10	US-09-934-323-1	1,
13	56.8	ω . ω	2191	9	US-09-954-531-1038	Sequence 1038, Ap
14	56.8	ω .ω	2191	10	US-09-880-107-3854	Sequence 3854, Ap
15	56.8	<u>ن</u> ن	2484	9	US-10-102-806-271	Sequence 271, App
16	55.4	3.2	1641	10	US-09-895-860-3	Sequence 3, Appli
17	55.4	3.2	2087	10	US-09-895-860-1	
18	55.4	3.2	2428	ø	US-09-418-176-1	
19	55.4	3.2.	2428	10	US-09-969-347-220	2

.2 3824 9 US-10-028-0722 3824 9 US-10-025-8552 3824 9 US-10-123-9042 3824 9 US-10-123-9042 3824 9 US-10-175-7462 3824 9 US-10-176-9182 3824 9 US-10-176-9182 3824 9 US-10-176-9182 3824 9 US-10-036-2142 3824 9 US-10-036-2142 3824 9 US-10-036-2142 3824 9 US-10-035-71982 3824 9 US-10-035-71982 3824 9 US-10-035-71982 3824 9 US-10-035-1142 3824 9 US-10-140-0022 3824 9 US-10-230-1602 3824 9 US-10-230-1602 3824 9 US-10-036-1602 3824 9 US-10-036-1602 3824 9 US-10-036-1602 3824 9 US-10-036-1602 3824 9 US-10-036-1302 3824 9 US-10-036-1302 3824 9 US-10-035-9588 .2 3824 9 US-10-035-9588	5.4 3.2 3824 9 US-10-028-072-541 Sequence 5.4 3.2 3824 9 US-10-121-049-541 Sequence 5.4 3.2 3824 9 US-10-123-904-541 Sequence 5.4 3.2 3824 9 US-10-123-904-541 Sequence 5.4 3.2 3824 9 US-10-175-746-541 Sequence 5.4 3.2 3824 9 US-10-176-918-541 Sequence 5.4 3.2 3824 9 US-10-036-214-22 Sequence 5.4 3.2 3824 9 US-10-036-214-22 Sequence 5.4 3.2 3824 9 US-10-035-719-22 Sequence 5.4 3.2 3824 9 US-10-035-719-22 Sequence 5.4 3.2 3824 9 US-10-035-719-22 Sequence 5.4 3.2 3824 9 US-10-230-133-209 Sequence 5.4 3.2 3824 9 US-10-142-114-541 Sequence 5.4 3.2 3824 9 US-10-230-138-209 Sequence 5.4 3.2 3824 9 US-10-230-138-209 Sequence 5.4 3.2 3824 9 US-10-142-119-541 Sequence 5.4 3.2 3824 9 US-10-230-138-209 Sequence 5.4 3.2 3824 9 US-10-230-138-209 Sequence 5.4 3.2 3824 9 US-10-230-338-209 Sequence 5.4 3.2 3824 9 US-10-035-958-22 Sequence 5.4 3.2 3824 9 US-10-035-958-22 Sequence 5.4 3.2 3824 9 US-10-035-958-22 Sequence 5.4 3.2 3824 9 US-10-123-262-541 Sequence 5.4 3.2 3824 9 US-10-035-958-22 Sequence	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21
-10-028-07 -10-123-045 -10-123-90 -10-175-74 -10-176-91 -10-176-91 -10-176-91 -10-176-91 -10-176-91 -10-176-91 -10-176-91 -10-137-88 -10-036-21 -10-140-47 -10-140-47 -10-143-11 -10-143-11 -10-230-136 -10-230-136 -10-230-33 -10-230-33 -10-230-33 -10-230-33 -10-230-33 -10-230-33 -10-230-33	.2 3824 9 US-10-028-072-541 Sequence 2 3824 9 US-10-121-049-541 Sequence 2 3824 9 US-10-121-049-541 Sequence 2 3824 9 US-10-123-904-541 Sequence 2 3824 9 US-10-123-904-541 Sequence 2 3824 9 US-10-176-918-941 Sequence 2 3824 9 US-10-27-884-209 Sequence 2 3824 9 US-10-137-865-541 Sequence 2 3824 9 US-10-137-865-541 Sequence 2 3824 9 US-10-137-451-92 Sequence 2 3824 9 US-10-135-719-22 Sequence 2 3824 9 US-10-140-474-541 Sequence 2 3824 9 US-10-143-114-541 Sequence 2 3824 9 US-10-143-114-541 Sequence 2 3824 9 US-10-143-114-541 Sequence 2 3824 9 US-10-230-163-209 Sequence 2 3824 9 US-10-230-163-209 Sequence 2 3824 9 US-10-218-631-209 Sequence 2 3824 9 US-10-218-631-209 Sequence 2 3824 9 US-10-218-631-209 Sequence 2 3824 9 US-10-230-338-209 Sequence 2 3824 9 US-10-036-150-22 Sequence 2 3824 9 US-10-036-958-22 Sequence 2 3824 9 US-10-133-262-541 Sequence	55.4	55.4	55.4	55.4	55.4	55.4	55.4	55.4	55.4	55.4	5	55.4	55.4	55.4	55.4	5	5	5	5	5	5	5	5	5	5
9 US-10-028-07) 9 US-10-121-04) 9 US-10-123-90, 9 US-10-175-74, 9 US-10-176-91; 9 US-10-176-91; 9 US-10-176-92; 9 US-10-137-86, 9 US-10-137-86, 9 US-10-137-86, 9 US-10-140-47, 9 US-10-140-47, 9 US-10-140-47, 9 US-10-140-47, 9 US-10-142-41, 9 US-10-142-43, 9 US-10-142-43, 9 US-10-143-11, 9 US-10-143-13, 9 US-10-143-13, 9 US-10-143-13, 9 US-10-143-13, 9 US-10-143-13, 9 US-10-143-14, 9 US-10-143-15, 9 US-10-143-16, 9 US-10-143-16	9 US-10-028-072-541 Sequence 9 US-10-035-855-22 Sequence 9 US-10-121-049-541 Sequence 9 US-10-123-904-541 Sequence 9 US-10-123-904-541 Sequence 9 US-10-176-746-541 Sequence 9 US-10-176-746-541 Sequence 9 US-10-176-918-541 Sequence 9 US-10-176-921-541 Sequence 9 US-10-137-865-541 Sequence 9 US-10-137-865-541 Sequence 9 US-10-137-865-541 Sequence 9 US-10-137-865-541 Sequence 9 US-10-140-474-541 Sequence 9 US-10-142-413-541 Sequence 9 US-10-142-413-541 Sequence 9 US-10-143-114-541 Sequence 9 US-10-143-114-541 Sequence 9 US-10-143-153-209 Sequence 9 US-10-218-631-209 Sequence 9 US-10-218-631-209 Sequence 9 US-10-218-631-209 Sequence 9 US-10-036-150-22 Sequence 9 US-10-036-150-22 Sequence 9 US-10-036-150-23 Sequence 9 US-10-036-150-23 Sequence 9 US-10-036-150-23 Sequence					•								٠		•			•	•					•	
US-10-028-07 US-10-121-04 US-10-123-90 US-10-123-90 US-10-175-74 US-09-91-83 US-10-176-92 US-10-176-92 US-10-176-92 US-10-176-92 US-10-176-92 US-10-176-92 US-10-140-47 US-10-142-43 US-10-143-11 US-10-143-11 US-10-143-11 US-10-143-13	US-10-028-072-541 Sequence US-10-035-855-22 Sequence US-10-121-049-541 Sequence US-10-1123-904-541 Sequence US-10-1123-904-541 Sequence US-10-1176-146-541 Sequence US-10-176-921-541 Sequence US-10-176-921-541 Sequence US-10-176-921-541 Sequence US-10-176-921-541 Sequence US-10-176-921-541 Sequence US-10-137-865-541 Sequence US-10-137-865-719-22 Sequence US-10-137-719-22 Sequence US-10-137-719-22 Sequence US-10-137-1542 Sequence US-10-136-131-541 Sequence US-10-136-160-22 Sequence US-10-142-431-541 Sequence US-10-142-631-209 Sequence US-10-143-114-541 Sequence US-10-141-541 Sequence US-10-141-541 Sequence US-10-141-541 Sequence US-10-141-541 Sequence US-10-131-541 Sequence US-10-131-541 Sequence US-10-231-338-209 Sequence US-10-33-338-209 Sequence US-10-133-262-541 Sequence	3824	3824	3824	3824	3824	3824	3824	3824	3824	3824	3824	3824	3824	3824	3824	3824	3824	3824	3824	3824	3824	3824	3824	3824	3824
-10-028-07 -10-123-045 -10-123-90 -10-123-90 -10-176-91 -10-176-91 -10-176-91 -10-176-91 -10-176-91 -10-176-91 -10-176-91 -10-137-88 -10-036-21 -10-140-47 -10-143-11 -10-143-11 -10-143-11 -10-230-16 -10-230-16 -10-230-33 -10-230-33 -10-230-33 -10-230-33 -10-230-33 -10-035-95 -10-035-95 -10-035-95 -10-035-95	-10-028-072-541 Sequence -10-121-049-541 Sequence -10-123-904-541 Sequence -10-123-904-541 Sequence -10-123-904-541 Sequence -10-176-918-541 Sequence -10-176-918-541 Sequence -10-176-918-541 Sequence -10-176-918-541 Sequence -10-176-921-541 Sequence -10-10-10-10-10-10-10-10-10-10-10-10-10-	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9
		-10-123-262-	-10-036-150-	-10-035-958-	-10-230-338-	-10-218-631-	-10-142-419-	-10-036-160-	-10-140-002-	-10-230-163	-10-143-114	-10-142-431	-10-035-719	-10-140-47	-10-137-86	-10-036-21	-10-227-88	-10-176-921	-10-176-918	-10-175-746	-09-931-836-	-10-140-470	-10-123-904	-10-121-049	-10-035-855-	-10-028-072-

## ALIGNMENTS

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US-10-083-590-13
; Sequence 13, Application US/10083590
; Publication No. US20030027257A1
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APPLICANT: IATROU, Kostas
APPLICANT: FARRELL, Patrick J.
APPLICANT: BEHIE, Leo A.
APPLICANT: BEHIE, Leo A.
TITLE OF INVENTION: SEQUENCES FOR IMPROVING THE EFFICIENCY OF SECRETION OF
TITLE OF INVENTION: NON-SECRETED PROTEINS FROM MAMMALIAN AND INSECT CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Pa
                                                                                                                                                                                                                                                                                                                       Query Match 5.2%;
Best Local Similarity 53.6%;
Matches 211; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-24
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-20
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PRIOR FILING DATE: 1997-08-21
NUMBER OF SEQ ID NOS: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 028722-207
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1691
TYPE: DNA
ORGANISM: Heliothis virescens
                                                                                                                                  428 ATCATCGTGATATGTATGGTCCTGATTATTCATTAAAAAAGGATGTGGTGTTGATTAACA 487
                                                                                                                                                                                                                                              368 CCGAAACTAAACGTCCCGTTTTAGTATACATACATGGTGGTGGTGTTTTATTATCGGTGAAA 427
500 TTAATTACAGATTGAACGTCTTCGGTTTCCTGTCCATGAACACAACACA-----AAAATCC
                                                488 TACAATATCGTTTGGGAGCTCTAGGTTTTCTAAGTTTAAATTCAGAAGACCTTAATGTGC 547
                                                                                                        440 GCCACGAGGACCTACACGGACCAGAATATTTGGTCACTAAGAATGTCATCGTCATCACGT 499
                                                                                                                                                                                                                 380 CCACACCTTTACGGCCTATCCTGGTGTTCATACATGGTGGAGGATTTGCTTTCGGCTCCG 439
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Pred. No. 5.9e-13;
0; Mismatches 177;
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US-09-738-626-1254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: KEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1254, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                           Query Match 4.6%;
Best Local Similarity 50.4%;
Matches 278; Conservative
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SEQ ID NO 1254
LENGTH: 1611
TYPE: DNA
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: NAKAGAWA, SATOSHI APPLICANT: MIZOGUCHI, HIROS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-08-03 NUMBER OF SEQ ID NOS: 7059
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                   414
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                                                                                                                                                                                                                                                                                           177 GGGTATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCACCCCAGCGACC
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TATTATCGGTGA---AAATCATCGTGATATGTATTGGTCCTGATTATTTCATTAAAAAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGAATTTCGGAGGAGCCCCAGCGACATCACCATAGCGGGGCAGAGCGCTGGTGCATCAG
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                                                 G-----CCTGATTCCGAAGAAAAGCTTCCTGTTGTGGTGTATCTCCACGGGGGTTCCTT
                                                                                  GTACTCCTGGACAGATAAGATTCGCGGTTCAGAAGACTGCCTTAACCTCGATGTCGTGCG
                                                                                                                                                       TGATTTTATAACGGGCAAAGTGTGTGGCTCAGAGGATTGTCTATACCTAAGTGTCTATAC
                                                                                                                                                                                         CAAGAAATGGGACGGCGTGCGCGATTGCTCAATGTTCGGTGAAGTAGCTTCTCAGCCAAC
                                                                                                                                                                                                                      AACACCCTGGGATGGTGTGCGCGATTGTTGCA---ATCATAAAGATAAGTCAGTGCAAGT 293
                                                                                                                                                                                                                                                           GGGAATTCCCTACGGCCGAAACACTGGCGGAAAATATCGCTTCCGGGCACCCCGGCCCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGAGCGGAACAGGAATGAGCTACTTCTTTACTAC 767
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SENOH, AKIHIRO
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                                                                                                                                                                                                                                                                                                                                             Score 78.8; DB 9; Pred. No. 2.3e-10;
                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                            DB 9;
                                                                                                                                                                                                                                                                                                                                                            Length 1611;
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APPLICANT: Lockridge, Oksana
APPLICANT: Watkins, Jeffry D.
TITLE OF INVENTION: Butyrylcholinesterase Var
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: P-1X 4143
CURRENT APPLICATION NUMBER: US/09/748,739A
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
SEQ ID NO 1
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; LOCATION: (86)...(1891)
US-09-748-739A-1
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US-09-748-739A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 190; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1967
TYPE: DNA
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                                          TTATTTGATCAACAGTTGGCTCTTCAGTGGGTTCAAAAAAATATAGCAGCCTTTGGTGGA
                                                              CTTAAAGATCAAGTCATGGGCTTGCGTTGGATTAAAAATAATTGCGCCAACTTTGGTGGC 621
                                                                                                                GGTGCCCTAGGATTCTTAGCTTT----GCCAGGAAATCCTGAGGCTCCAGGGAACATGGGT 670
                                                                                                                                                   GGAGCTCTAGGTTTTCTAAGTTTAAATTCAGAAGACCTTAATGTGCCCGGTAATGCCGGC 561
                                                                                                                                                                                          GATGGCAAGTTTCTGGCTCGGGTTGAAAGAGTTATTGTAGTGTCAATGAACTATAGGGTG
                                                                                                                                                                                                                      GGTCCTGATTATTCATTAAAAAAGGA----TGTGGTGTTGATTAACATACAATATCGTTTG 501
                                                                                                                                                                                                                                                                    GTATTGATATGGATTTATGGTGGTGGTTTTCAAACTGGAACATCATCTTTACATGTTTAT
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 AATCCCGATAATATTACAGTCTTTGGTGAAAGTGCCGGTGCTGCCTC
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APPLICANT: Lockridge, Oksana
APPLICANT: Watkins, Jeffry D.
APPLICANT: Watkins, Jeffry D.
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: P-IX 4143
CURRENT APPLICATION NUMBER: US/09/748,739A
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 31
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US-09-748-739A-3
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US-09-880-107-2271
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                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                   Sequence 3, Application US/09748739A Patent No. US20020119489A1
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Best Local Similarity 54.8%;
Matches 190; Conservative
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PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
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TITLE OF INVENTION: Gene Expression Profiles
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
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TYPE: DNA
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Pred. No. 6e-06;
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; NAME/KEY: CDS
; LOCATION: (214)...(1935)
US-09-748-739A-5
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                                                                                                                                                                                                                                                           SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 2416
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US Patent No. US20020119489A1 GENERAL INFORMATION:
                                                                 Query Match
Best Local Similarity
Matches 190; Conserv
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                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: P-IX 4143
CURRENT APPLICATION NUMBER: US/09/748,739A
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEO ID NOS: 31
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lockridge, Oksana
APPLICANT: Watkins, Jeffry D.
TITLE OF INVENTION: Butyrylcholinesterase Variants
TITLE OF INVENTION: Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ
                                                                                                                                                                                                      FEATURE:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: CDS
LOCATION: (214)...(1935)
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ORGANISM: Artificial Sequence
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                                                                  Conservative
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54.8%;
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                                                                 Score 62.2; DB 10;
Pred. No. 6e-06;
0; Mismatches 148;
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Sequence 7, Application US/09748739A Patent No. US20020119489A1 GENERAL INFERMATION:

APPLICANT: Lockridge, Oksana APPLICANT: Watkins, Jeffry D.

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775 AATCCTAAAAGTGTAACTCTCTTTGGAGAAAGTGCAGGAGCAGCTTC 821

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CURRENT APPLICATION NUMBER: US/09/748,739A
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Butyrylcholinesterase Variants TITLE OF INVENTION: Methods of Use FILE REFERENCE: P-IX 4143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Human Butyrylcholinesterase
                                                                                                                                                                                                                                                                                                                                                                                     481 GAAGACTGTTTATATCTAAATGTATGGATTCCAGCACCTAAACC---AAAAAATGCCACT 537
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622 AATCCCGATAATATTACAGTCTTTGGTGAAAGTGCCGGTGCCTC
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                                                                                   CTTAAAGATCAAGTCATGGCCTTGCGTTGGGATTAAAAATAATTGCGCCAACTTTTGGTGGC 621
                                                                                                                                                                                 GGAGCTCTAGGTTTTCTAAGTTTAAATTCAGAAGACCTTAATGTGCCCGGTAATGCCGGC 561
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                                                                                                                                                                                                                                                                                                                                               GITTTAGTATACATACATGGTGGTGGTGGTTTTATTATCGGTGAAAATCATCGTGATATGTAT 444
                                                                                                                                          GGTGCCCTAGGATTCTTAGCTTT---GCCAGGAAATCCTGAGGCTCCAGGGAACATGGGT
                                                           TTATTTGATCAACAGTTGGCTCTTCAGTGGGTTCAAAAAAATATAGCAGCCTTTGGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 62.2; DB 10;
pred. No. 6e-06;
0; Mismatches 148;
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US-09-748-739A-16
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SOFTWARE: Fasts
SEQ ID NO 16
FRIGTH: 2416
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Best Local Similarity 54.8%;
Matches 190; Conservative
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APPLICANT: Watkins, Jeffry D.
TITLE OF INVENTION: Butyrylcholinesterase Variants
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: P-IX 4143
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CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
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TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                       APPLICANT: ANADYS PHARMACEUTICALS, INC
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                                                                                                                                                                                                        HARRIS, Sandra
                                                                                                                                                                                                                         BRADLEY, John
DESILVA, Thamara
                                                                                                                                                                                                                                                              BUURMAN, Ed T.
                                                                                                                                                                                                                                                                                         MOORE, Jeffrey
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                                                                               HAQ, Tariq
                                                                                                      SANDERSON, Karen
                                                                                                                       MCCOY, Melissa
                                                                                                                                        MOORE,
                                                                                                                                                              MENDILLO, Marc
                                                                                                                                                                                   KOMARNITSKY, Svetlana
                   DAVIDOV, Eugene
                                                             ZHU, Shuhao
                                          LONG,
                                          Fan
                                                                                                                                            Daniel
                                                                                                                                                                                                                                                                                                             Craig
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Pred. No. 6e-06;
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561 657 501

; NAME/KEY: CDS ; LOCATION: (214)...(1935) US-09-748-739A-7

ORGANISM: Artificial Sequence

FEATURE: FEATURE:

LENGTH: 2416 TYPE: DNA

ID NO 7

Query Match Matches

Local

3.6%; al Similarity 54.8%; 190; Conservative

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TYPE: DNA
ORGANISM: HOMO SAPIENS
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Human Genbank/NM_000055
DATABASE ENTRY DATE: 2001-02-03
RELEVANT RESIDUES: (1)..(2444)
US-09-893-519A-112
S
                                                                                                                                                                                                                                                                                                                                                                                                          US-09-974-300-1107
Sequence 1107, Application US/09974300; Patent No. US20020146721A1; GENERAL INFORMATION:
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                                                                                                                                              TITLE OF INVENTION: Methods For Monitoring No TITLE OF INVENTION: Expression FILE REFERENCE: 10085.500-US CURRENT APPLICATION NUMBER: US/09/974,300 CURRENT FILING DATE: 2001-10-05 PRIOR APPLICATION NUMBER: 09/680,598 PRIOR APPLICATION NUMBER: 09/680,598 PRIOR APPLICATION NUMBER: 60/279,526 PRIOR APPLICATION NUMBER: 60/279,526 PRIOR APPLICATION NUMBER: 60/279,526 PRIOR APPLICATION NUMBER: 60/279,526 PRIOR FILING DATE: 2001-03-27
                                                                                   NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1107
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Best Local :
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TYPE: DNA
ORGANISM: Bacillus licheniformis
-09-974-300-1107
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                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Berka, Randy M. APPLICANT: Clausen, ib Groth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.1
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                                                             LENGTH: 657
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Local Similarity 54.8%;
hes 190; Conservative
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Pred. No. 6.1e-06;
0; Mismatches 148;
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US-09-934-323-3
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                                                                                                                                                                                                                                                                                   Best Local Similarity 54.2
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 3
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Best Local Similarity
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TITLE OF INVENTION: 33410, A MOVEL HUMAN CARBOXYLESTERASE

TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF

FILE REFERENCE: 10448-081001

CURRENT APPLICATION NUMBER: US/09/934,323

CURRENT FILING DATE: 2001-08-21

PRIOR APPLICATION NUMBER: US 60/226,774

PRIOR APPLICATION NUMBER: US 60/226,774

PRIOR APPLICATION NUMBER: US 60/226,774

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo
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851 TCCAGAAGGCCATCGCCCAGAGTGGCACCGCCATTT 886
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                                                                                                   650 AAAGTGCCGGTGCTGCCTCTACCCCACTACATGATGTTAACCGAACAAACTCGCGGTCTTT
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                                                                                                                                                           GGATTAAAAATAATTGCGCCAACTTTGGTGGCAATCCCGATAATATTACAGTCTTTGGTG
                             TCCATCGTGGTATACTAATGTCGGGTAATGCTATTT 745
                                                                   CCGGGGCAGGGGCCTCCTGCGTCAACCTTCTGATCCTCTCCCACCATTCAGAAGGGCTGT
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Pred. No. 4e-0!
0; Mismatches
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Pred. No. 9
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4e-05;
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RESULT 12 US-09-934-323-1

Sequence 1, Application US/09934323 Patent No. US20020150910A1

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; NAME/KEY: CDS
; LOCATION: (420)...(2924)
US-09-934-323-1
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APPLICANT: CUILLS, ROTY A. J.
APPLICANT: CUILLS, ROTY A. NOVEL HUMAN CARBOXYLESTERASE
TITLE OF INVENTION: 33410, A NOVEL HUMAN CARBOXYLESTERASE
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
TILLS PRICATION (MUMBER: US/09/934,323
CURRENT FILING DATE: 2001-08-21
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/226,774
PRIOR FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FRSELSEQ for Windows Version 4.0
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Best Local
                                                         ; ORGANISM: HOMO
US-09-954-531-1038
                                                                                                                                                                                                                                        TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand Title OF INVENTION: Gene Sets FILE REFERENCE: 608290-77 CURRENT APPLICATION NUMBER: US/09/954,531 CURRENT FILING DATE: 2002-05-02 CURRENT FILING DATE: 2000-09-18 PRIOR FILING DATE: 2000-09-18 PRIOR FILING DATE: 2000-09-20 PRIOR APPLICATION NUMBER: US/60/234,009 PRIOR APPLICATION NUMBER: US/60/234,509 PRIOR APPLICATION 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1038, Application US/09954531 Patent No. US20020165180Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION: APPLICANT: Weaver,
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TYPE: DNA
ORGANISM: Homo sapiens
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Query Match
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                                                                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 1392
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                                                                                                                     TYPE:
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Pred. No. 0.00014;
                  Score
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                                                                                                                                                                                                                                      , OTHER INFORMATION: Genbank accession No. US20020142981A1 v09616 US-09-880-107-3854
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                                                                                                                                                                                                                                                                                                                       SEQ ID NO 3854
LENGTH: 2191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles
FILE REFERENCE: 44921-5028-WO
                                                                                                                                                                                           Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
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                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/237,054 PRIOR FILING DATE: 2000-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/211,379 PRIOR FILING DATE: 2000-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Horne,
                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2000-10-02 NUMBER OF SEQ ID NOS: 3950
                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver.
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CGTCCCGTTTTAGTATACATACATGGTGGTGGTGTTTATTATCGGTGAAAATCATCGTGAT 438
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0; Mismatches 177;
                                                                                                                                                                                                    Score 56.8; DB 10; pred. No. 0.00015;
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RESULT 15
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Sequence 271, Application US/10102806
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                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (194)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (623)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (2396)
OTHER INFORMATION: n equals a,t,g, or c
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SEQ ID NO 271
LENGTH: 2484
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Best Local :
                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 09/925,298
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/102,806
CURRENT FILING DATE: 2002-03-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rosen et al.
                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature LOCATION: (2484)
                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: n equals a,t,g, or c
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                                    1068 ATGATGGTTCCATGCTGGCTGCCT-TGGAGAACGTGGTGGTGGTCATCATCCAGTACCGC 1126
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499 TTGGGAGCTCTAGGTTTTCTAAGTTTAAATTCAGAAGACCTTAATGTGCCCCGGTAATGCC 558
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                                                                                                                CTGCCGGTGATGGTGGATCCACGGTGGTGCGCTTGTTTTTG--GCATGGCTTCCTTGT 1067
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                                                                           ATGTATGGTCCTGATTATTTCATTAAAAAGGATGTGGTGTTGATTAACATACAATATCGT 498
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Pred. No. 0.00016;
0; Mismatches 177;
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                         ATGATGTTAACCGAACAAACTCGCGGTCTTTTCCATCGTGGTAT 722
                                                     GGCAACCCTGACCGTGTCACCATTTTTGGCGAGTCTGCGGGTGGCACGAGTGTGTCTTCG 1300
                                                                      GGCAATCCCGATAATATTACAGTCTTTGGTGAAAGTGCCGGTGCTGCCTTACCCACTAC
                                                                                                         GGCTACCTGGACCAAGTGGCTGCACTACGCTGGGTCCAGCAGAATATCGCCCCACTTTGGA 1240
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Search completed: April 11, 2003, 13:23:30 Job time: 105.528 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first, 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

ORGANISM REFERENCE AUTHORS	VERSION KEYWORDS SOURCE	RESULT AR153440		44	4 4 3 2	44	u	37	ა ა თ თ	34.	32	30 31	29	27	26 26	24	22 23	21			c 16		13	11	10	o <b>co</b> ·	7 6	ν Cπ .	ω 4	2	Result No.
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, Campbell,P.Malcolm., audianos,C., Smyth,KA., and Brownlie,J.Colin.		linear PAT 08-AUG-2001		, m	ulex p	Sol	dosc	AF216216 Drosophil	)rosophila	AE003671 Drosophil	rosophi	sophila rosophi	z47988 C.quinquefa	rosophi	rosophi	rosophi	AC014297 Drosophil AC008098 Drosophil	rosophi	rosophi	rosophi	ACCOUNTY Drosophil	U51050 Drosophila	AY121675 Drosophil	equence	AF133341 MUSCA COM AF139082 Haematobi	equenc	equenc	AR062837 Sequence	equenc	AR153440 Sequence AR153442 Sequence	Description

RESULT 1	
AR153440	
LOCUS	AR153440 1713 bp DNA linear PAT 08-AUG-2001
DEFINITION	Sequence 5 from patent US 6235515.
ACCESSION	AR153440
VERSION	AR153440.1 GI:15120972
KEYWORDS	•
SOURCE	Unknown.
ORGANISM	Unknown.
	Unclassified.
REFERENCE	1 (bases 1 to 1713)
AUTHORS	Russell, R. Joyce., Newcomb, R. David., Campbell, P. Malcolm.,
	Robin, G.Charlesde. Quetteville., Claudianos, C., Smyth, KA.,
	Boyce, T. Mark., Oakeshott, J. Graham. and Brownlie, J. Colin.
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Sequence 9
AR153442
AR153442.1
         Unclassified.
1 (bases 1 to 1713)
1 (bases 1 to 1713)
Russell, R.Joyce., Newcomb, R.David., Campbell, P...
Robin, G. Charlesde. Quetteville., Claudianos, C.,
Boyce, T. Mark., Oakeshott, J. Graham. and Brownlie
Malathion carboxylesterase
Patent: US 6235515-A 9 22-MAY-2001;
                                                                          Unknown
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Location/Qualifiers
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Query Match Best Local

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TITLE JOURNAL FEATURES

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1 (bases 1 to 1713)

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Russell, R.Joyce, Newcomb, R.David., Campbell, P.M.

Russell, Charlesde. Quetteville, Claudianos, C., S.

Robin, G. Charlesde. Quetteville, Candam. and Brownlie,

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Russell,R.Joyce., Newcomb,R.David.,
Boyce,T.Mark., Campbell,P.Malcolm.,
Oakeshott,J.Graham. and Smyth,K.-A.
Enzyme based bioremediation
Patent: US 5843758-A 1 01-DEC-1998:
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Location/Qualifiers

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1 (bases 1 to 1713)

1 (bases 1 to 1713)

Russell, R. Joyce., Newcomb, R. David., Campbell, P. M. Russell, R. Joyce., Septimental Candianos, C., S. Robin, G. Charlesde. Quetteville., Claudianos, C., S. Boyce, T. Mark., Oakeshott, J. Graham. and Brownlie, Malathion carboxylesterase patent: US 6235515-A 7 22-MAY-2001;
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Russell,R.Joyce., Newcomb,R.David., Rc
Boyce,T.Mark., Campbell,P.Malcolm., Pa
Oakeshott,J.Graham. and Smyth,K.-A.
Enzyme based bioremediation
Patent: US 5843758-A 2 01-DEC-1998;
Location/Qualifiers
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'Organism="unknown"

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       GTCTACTTGTATCGCTTCGACTTCGACTTCGGAGGATCTTATCAATCCCTATCGTATTATG
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Musca domestica carboxylesterase MdaE7 (
AF133341 GI:4768932
                                                                                                                                       Insect B: 99381228
                                                                                                                                               Claudianos, C., Russell, R.J. and Oakeshott, J.G. The same amino acid substitution in orthologous esterases organophosphate resistance on the house fly and a blowfly Insect Biochem. Mol. Biol. 29 (8), 675-686 (1999)
                                                                                                                                                                                  Musca domestica
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Muscoidea; Muscidae; Musca
1 (bases 1 to 2160)
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Submitted (07-MAR-1999) Entomology,
ACT 2601, Australia
                                                                                                            Claudianos, C.,
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        /strain="Rutgers Diazinon-R
/db_xref="taxon:7370"
/chromosome="II"
/dev_stage="4 day third inst
1. .2160
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/gene="MdaE7"
                                                      /organism="Musca domestica"
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AATATTGCCAATTTCGGTGGCGATGTAGACAATATTACCGTCTTCGGCGAAAGTGCTGGT
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VKRMTYYDDSYYSFESIPYAKPPVGELRFKAPQRPVPWEGDKINKFGPDYFMKKPVVL
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AGGASTHYMMITEQTRGLFHRGIMMSGNSMCSWASTECQSRALTMAKRVGYKGEDNEK
BILEFLMKANPYDLIKEEPQVLTPEEMQNKVMFPFGPTVEPYQTADCVVPKPIREWYK
SAWGNSIPTLIGNTSYEGILFKSIAKQYPEVVKELESCVNYVPWELADSERSAPETLE
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EEIINPYRIMRFGRGVKGVSHADELTYLFWNILSKRLPKESREYKTIERWGJWTEEA
TTGKPYSNDIAGMENLTWDPIKKSDDVYKCLNIGDELKVMDLPEMDKIKGWASIFDKK
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/EC_number="3.1.1.1"
/note="mutant ali-esterase; similar to the Lucilia cuprina aE7 alpha esterase; organophospate resistance"
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                                                          ATCGGCGATGAATTGAAAGTTATGGATTTGCCAGAAATGGATAAAATTAAACAATGGGCA
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Guerrero,F.D.

Cloning of a horn fly cDNA, HialphaE7, encoding an esterase transcript concentration is elevated in diazinon-resistant f Insect Biochem. Mol. Biol. 30 (11), 1107-1115 (2000)
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Direct Submission
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/gene="aE7"
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GNSSGSEDCLYLNYTNIKLNTDTKRPVLVFFHGGFICGANRNYYGADFIKRVDYF
ITVQYRLGVLGFISLNSENLNYPGNAGLKCDVYAALRWIKNCASFGGDPDCITLFGES
AGAASTHYMMITEQARGLFHRAVLMSGTAMCIWAHTQCQHRGYTIAKRIGYKGENNDK
DVYDFLMKANPYDLAREBHKVLINEBLBDKVWFAFGFTEPYETPDCVLFKPNREMLK
TAWGNSIPTLIGUTSYEGLLFISVGKONPHLIKELETFECYVPGELVVEDRSPESLE
TASILKKLYVRGETPTLESFTELCSDFYFWYDHRFLQLRFNHTYGSPIYLYRRDEDS
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/strain="Camp Cooley 4,97"
/sub_species="irritans"
/db_xref="taxon:75445"
/clone="HF41CC"
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/protein_id="AAF14517.1"
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Russell,R.Joyce., Newcomb,R.David., Campbell,P.Malcolm.,
Russell,R.Joyce., Newcomb,R.David., ClaudianoS,C., Smyth,K.-A.,
Robin,G.Charlesde.Quetteville., ClaudianoS,C., Smyth,K.-A.,
Boyce,T.Mark., Oakeshott,J.Graham. and Brownlie,J.Colin.
Boyce,T.Mark., Oakeshott,J.Graham. and Brownlie,J.Colin.
Malathion carboxylesterase
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Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J., Chawez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Li, P., Liao, G., Miranda, A., Mungall, C.J., Nunco, J., Pacleb, J., Paragas, V., Park, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M. and Celniker, S.
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Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
                                                                                                              reflect accurately this particular cDNA clone. However, there are artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAs, and reverse transcriptase errors that result in single base changes.
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1 (bases 1 to 2017)
                                             For further information about this sequence, including its location and relationship to other sequences, please visit our Web site (http://fruitfly.berkeley.edu) or send email to
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Berkeley, CA 94720
This clone was sequenced as part of a high-throughput process to
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Sequence submitted by:
Berkeley Drosophila Genome Project
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/strain="y; cn bw sp"
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AAGGAATTGGAAACTTGTGTCAATTTTGTGCCAAGTGAATTGGCTGATGCTGAACGCACC
                               GGAAACTCCTTCGAAGGTCTCCTCATGTTTCCCGAAGTGAACAAGTGGCCGGAACTGCTT
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                                                                                                                                                                 ACCATGTTCAGCTTTGGACCCACCATCGAGCCCTATTTGACTCCTCATTGTGTGATTCCC
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Drosophila melanogaster
Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                  Submitted (11-MAR-1996) Charles Entomology, Clunies Ross Street,
                                                                                                                                               Robin,C., Medveczky,K.M., Russell,R.J. and Dupilcation and Divergence of the genes of cluster of Drosophila melanogaster J. Mol. Evol. (1996) In press
                                                                                                                                                                                                                                                                                                  Drosophila melanogaster
U51050
                                                                                                              Direct Submission
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                                    /organism="Drosophila
/db_xref="taxon:7227"
           /map="84D3"
                         'Chromosome="3R"
                                                                        ocation/Qualifiers
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                                                                                 Robin, Biotechnology, CSIRO div., Canberra, ACT 2601, Australia
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GLFHRGILQSGSAICPWAYNGDITHNPYRIAKLVGYKGEDDNCDVLGFLQNVKAKDL;
RVEENVLTLEERNNKIMFRFGPGSLEPFSTPECVISKPPKEMMKTAWSNSIPMFIGNTS
YEGLLAVPEVKLMPQVLQQLDAGTPFIPKELLATEPSKEKLDSWSAQIRDVHRTGSES
TPDNYMDLCSIYYFVFPALRVVHSRHAKAAGAPVFYKYDFDSEELIFPYRIMRWGRG
VKGVSHADDLSYGFSSLLARRLPKESREYKNIERTVGFAATGNPYSEKINGMDT
LTIDPVRKSDEVIKCLNISDDLKFIDLPEWPKLKVWESLYDDNKDLLF*
609 c 657 g 776 t 1 others
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/protein_id="AAB01149.1"
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                                                                                                             GGTCAGCCATGCCGACGATTTGAGCTACCAATTCAGCAGCCTGCTGGCTCGCCGGTTGC
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                                                       CGAAGGAAAGTCGCGAGTACAGGAACATCGAACGAACCGTGGGCATCTGGACCCAGTTTG
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Best Local Similarity
Matches 1051; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rockville, MD, USA
This sequence was identified as CDM:10213452 by
For further information on this sequence e-mail
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is avai
* the accession number will be preserved.
1. 57335
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 57335)
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Drosophila melanogaster.
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Drosophila melanogaster, ***
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0; Mismatches 615
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Qy 1098 TANGGARTING Db 35221 GCAGCAGCTTG Qy 1158 CGCCCAAGAG Qy 1158 CGCCCAAGAGA Db 35161 TANAGAAAAAC Qy 1218 ACCAACAGCTC Qy 1218 ACCAACAGCTC Db 35101 AAGCACCCCAC Qy 1243	35401 1040 35341 1059 35281	Qy 860 CACAGGAT  Db 35521 CCAAGGAT  Oy 920 TCATGTTT  Db 35461 TAATGTTT  Db 35461 TAATGTTT	Oy 743 TTTGTCCATTGGC-	1 TCAAGG	501 ( 35941 ) 510 35881	Qy 361 Db 36121 GTAATAACTTTI Qy 381 TCCCGTTTTAG' Qy 381 TCCCGTTATGG' Qy 441 GTATGGTCCTG Qy 441 GTATGGCCCCGG Db 36001 GTATGGCCCCGG
TIGGAACC TIGATGC AGACCTT ACTGGA ACTGATAA               CCTGATAA   CAGATAA	AGCCTCCAAAGGAGATGATGAAGACCGCCTGGAGTAACTCCATCCCCAACAGCTCCAAAAGGAGATGAAGACAGCCCTGGAGTAACTCCATCCCAACACTACAATATGAAGGATCTAAACTTTAAGCAAATTTTAAGCAAATTTTAATTTCAACAGAAGTAAATTTAAATTTTAATTTCAACAGAAGTGAAATTGGCTTAAGCAAATTTCAAATTAATT	TTAGTAAACTTORGEAMANT TTAGTAAAACTTORGEAMAAA CTTATTCGCGTGGAGGAAAAA CCCTTTTTGGCTCCACTGTGAC THILL THILL TORGEAMATGGTTAAAACTGC	TTGGCTAATACCCAATGT	AGGTGCTGGCCCTCAAGTGGI AGGTGCTGGCGAAI ATATTACAGTCTTTGGTGAAI IGCATCACTGTTTTTGGAGAGI BAACAAACTCGCGGTCTTTCC JAIL	GGAGCTCTGGAGCTCT-GCGTA GGGGCTTTGGGCTAATCTACTGTGAAATTCAGAGGTTTTCTAAGTTTAAATTCAG	CTTTAAACATTTTTATTTGTGGTACATTTTAGGTGAAACCGI TTAGTATACATACATGGTGGTGGTGCTTTTATTGTGGTGAAAATC. TTAGTATACATACATGGTGGTGGTGGTTTTATTATCGGTGAAAAATC.
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ACGGAGCCAG 35162 ACAGGAGAAC 1217               ACTGGCTCAGA 35102	TTTATAGAA		AAGG 91	TCGGCGGAG 35762 TCGGCGGAG 35762 ACTACATGA 682 ACTACATGA 35702 ACTACATGA 35702 GTAATGCTA 742 GTATGCTA 35642	A 62 35	AAGGCTCG 36062 AAGGCTCG 36062 CGGGAATG 36002 CGGGAATG 36002 TATCGTT 500

Search completed: April 11, 2003, 06:04:13 Job time : 3017.03 secs

Qy Db 3	Qy :	Qy 1	Qy 1 Db 34	Qy 1 Db 34	Oy 1 Db 34		Qy 17	Db 350
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	ATGTTTGAAAAACATAGAG 1/02 	AGTGATGAATTGAAAATGA 1042	AAAATGTTTCCTGGGATC 1502	GTATATGGATACAATTT6 1322 GTATATGGATCCCAGTTTG 34742 GCATCTGGACCCAGTTTG 34742				HILL I

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Result
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                              OP-sensitive ester LC-alpha E7 malath OP-resistant ester Md-alpha-E7 gene.
                                                                                                                                                                                                                                                                                             Description
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AAQ91561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ91561 standard; cDNA; 1713 BP
                                                                                                                                                                                                           13-JAN-1995;
                                                                                                                                                                                                                                                                  20-JUL-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lucilia cuprina
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Ctenocephalides fe	AAD21169	22	1590	8.4	143.8	45	
C. felis esterase,	AAV40743	19	1590		143.8	44	
. felis es	AAV40767	19	1488		143.8	43	
	ABL01946	23	4283	٠	152.8	42	
Drosophila melanog	ABL02029	23	1783	9.5	162	41	
Drosophila melanog	ABL01942	23	4288		166	40	
ă	AAD21174	22	2007		181.2	39	
esterase	AAV40755	19	2007	•	181.2	38	(3
esterase	AAV40754	19	2007	•	181.2	37	
esterase	AAV40757	19	1584	•	181.2		•
terase	AAV40756	19	1540	•	181.2	35	
esterase	AAV40765	19	1590	•	189		13
Ф	AAV40764	19	1590		189	33	
Drosophila melanog	ABL01858	23	5132	•	190.2	32	
Drosophila melanog	ABL01945	23	1626		192.8	31	
Drosophila melanog	ABL19064	23	2613	•	193.2	30	
Drosophila melanog	ABL02100	23	4294	•	197.2	29	
Drosophila melanog	ABL02098	23	4294		197.2	28	
terase	AAV40763	19	1987	•	199.2		()
Φ	AAV40762	19	1987	•	199.2	26	
Ω.	ABL02080	23	5008	•	220.8	25	
la	ABL01943	23	1727		228	24	
la	ABL02102	23	4242	•	230.2	23	
Drosophila melanog	ABL04688	23	4320	•	236.6		()
la	ABA90480	24	1809	•	271.6	21	
Drosophila melanog	ABL07668	23	67279		298.8	20	
rosophila	ABL10332	23	3856	•	298.8	19	
la	ABL02101	23	1719	•	304.2	18	
<u>l</u> a	ABL01947	23	1878	•	309.4	17	
la	ABL10333	23	1791		309.8	16	
la	ABL01859	23	1863	•	321.4	15	
_	ABL02103	23	1593	•	325.2	14	
la	ABL04689	23	1792		362.2	13	
la me	ABL02099	23	1665		366.6	12	
sophila	ABL02066	23	6175	21.5	369	11	
Drosophila melanog	ART.02081	23	1704		378.6	10	

## ALIGNMENTS

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Boyce TM,
Parker AG,
                                                                                                                                                                             Esterase; E3; bioremediation; organophosphate; carbamate; insecticide; pesticide; water decontamination; meat decontamination;
                                                                                                                                                                                                        OP-sensitive esterase E3 Lc743 clone.
                                                                                                                                                                                                                          22-DEC-1995 (first entry)
                          (CSIR ) COMMONWEALTH SCI & IND RES ORG.
Campbell PM, Newcomb RD, Oakes, Robin GC, Russell RJ, Smyth K;
                                           94AU-0003347.
                                                             95WO-AU00016
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                                                                                                                                                                                                                                                                                                                                                                                                Pure E3 esterase from Lucilia cuprina and related DNA - used to eliminate residues of organo:phosphate and carbamate pesticides water, meat etc.
                                                                                                                                                                                                                                                                                                                                                 cDNA from organophosphate (OP)-sensitive L. cuprina pupa cDNA library was amplified using cluster-specific esterase primers. Isolated clone LC743, a probable full-length cDNA, was expressed using a baculovirus vector in insect cells and shown to encode an OP-susceptible E3 esterase, useful in bioremediation.
                                                                                                                                                                                                                                                                                                                                                                                      Claim 5;
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P-PSDB; AAR78142.
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                                                                                                                                                                                                                                         Similarity
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RESULT 2
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Lc-alpha-E7

malathion

susceptible esterase clone

Lc743

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Query Match
Best Local Similarity
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                                                                       resistant enzyme acts as a malathion carboxylesterase and can be formulated for use in degrading environmental carboxylester or dimethyl general organophosphates.
                                                                                                                                              DNA molecule Lc743 (AAT68596) codes for an esterase (AAW17765) fa malathion susceptible strain of Lucilia cuprina. Comparison with a consensus sequence from derived from clones of the Lc-alpha-E7 resistant allele (see also AAW17768) indicated only replacement site difference, a Trp to Leu substitution at amino acid position 251 (nucleotide position 752). This mutation is a excellent candidate for the malathion resistance mutation. The
                                                                                                                                                                                                                                                                                                    Claim
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                                                                                                                                                                                                                                                                                                                                       DNA encoding enzyme that degrades organophosphate pesticides useful for decontamination of soil, water, food etc
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remediation; bioremediation; decontamination;
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                                   GCTGCCTCTACCCACTACATGATGTTAACCGAACAAACTCGCGGTCTTTTCCATCGTGGT
                                                                                                                                                                                                                                                          AATTGCGCCAACTTTGGTGGCAATCCCGATAATATTACAGTCTTTGGTGAAAGTGCCGGT
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                                                                                                           TTCACCTTAGCCAAATTGGCCGGCTATAAGGGTGAGAATAATGATAAGGATGTTTTGGAA
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Esterase; E3;
insecticide; |
                                                                                                                       OP-resistant
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                                                                                                                                                               AAQ91566 standard;
                                                                              Lucilia
13-JAN-1994;
             13-JAN-1995;
                                        WO9519440-A1
                          20-JUL-1995
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                                                                               cuprina
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eliminate
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RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding OP-susceptible esterase E3 of L. cuprina) from a diazinon resistant strain, Llandillo 103. 4 Isolated clones were sequenced (Lc7L103 A-D, AAQ91562-65) that encoded diazinin-resistant esterases; a consensus sequence is given in AAQ91566.
ATGAATTTCAACGTTAGTTTGATGGAGAAATTAAAATGGAAGATTAAATGCATTGAAAAT
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Robin GC, Russell RJ,
                                            97.9%;
nilarity 98.7%;
Conservative
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                                                                                                                                                           CGTAGTGGACGTGGTGTTAAGGGTGTTAGTCATGCTGATGAATTAACCTATTTCTTCTGG
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RESULT 4
AAQ91564
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Best Local Similarity Matches 1689; Conserv
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pure E3 esterase from Lucilia cuprina and related DNA eliminate residues of organo:phosphate and carbamate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lucilia
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insecticide; |
                                                                                                                                                                                                                                                                                                                                        Sequence 1713 BP;
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                                                            RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding OP-susceptible esterase E3 of L. cuprina) from a diazinon resistant strain, Llandillo 103. 4 Isolated clones were sequenced (Lc7L103 A-D, AAQ91562-65) that encoded diazinin-resistant esterases. The esterases, or cells expressing them, are used
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eliminate residues
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                                     GAAGAGCGTACAAATAAGGTCATGTTTCCTTTTGGTCCCACTGTTGAGCCATATCAGACC
                                                            TTTCTTATGAAAGCCAAGCCACAGGATTTAGTAAAACTTGAGGAAAAAGTTTTAACTCTA
                                                                                  GGTGAAAATCATCGTGATATGTATGGTCCTGATTATTTCATTAAAAAGGATGTGGTGTTG
                                                                                                                                                                                                                                            AAAGTGAAAGGCGTTAAACGTTTAACTGTGTACGATGATTCCTACTACAGTTTTGAGGGT
                                                                                                                                                                                                                                                                                                                                                           AAGTTTTTAAACTATCGTTTAACTACCAATGAAACGGTGGTAGCTGAAACTGAATATGGC
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 ATACCCACTATGATGGGTAACACTTCATATGAGGGTCTATTTTTCACTTCAATTCTTAAG
                      GCTGATTGTGTCTTACCCAAACATCCTCGGGAAATGGTTAAAACTGCTTGGGGTAATTCG
                                                                                                                                                                                  AATGTGCCCGGTAATGCCGGCCTTAAAGATCAAGTCATGGCCTTGCATTGGATTAAAAAT
                                                                                                                                                                                                ATTAACATACAATATCGTTTGGGAGCTCTAGGTTTTCTAAGTTTAAATTCAGAAGACCTT
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1689; Conservative
                 GCTGATTGTCTTACCCAAACATCCTCGGGAAATGGTTAAACATGCTTGGGGTAATTCG
                                                                                                                                                                            AATGTGCCCGGTAATGCCGGCCTTAAAGATCAAGTCATGGCCTTGCGTTGGATTAAAAAT
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      13-JAN-1995;
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                                                             Lucilia
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                                                                                                 Esterase; E3;
insecticide;
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WO9519440-A1
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                                                                                                                                                                                                                                                       GTCTACTTGTATCGCTTCGACTTCGATTCGGAAGATCTTATCAATCCCTATCGTATTATG
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                                                                cuprina
                                                                                                                                                                                                   standard;
                                                                                                 bioremediation;
pesticide; water
                                                                                                                                  esterase Lc7L103B
                                                                                                                                                       (first
                   Location/Qualifiers
1..1713
/*tag= a
                                                                                                                                                                                                   cDNA; 1713
                                                                                                                                                      entry)
                                                                                                  organophosphate;
decontamination;
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                                                                                                                                  allele
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                                                                                                  carbamate;
meat decor
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Best Local Similarity 98.5
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pure E3 es
eliminate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding OP-susceptible esterase E3 of L. cuprina) from a diazinon resistant strain, Llandillo 103. 4 Isolated clones were sequenced (Lc7L103 A-D, AAQ91562-65) that encoded diazinin-resistant esterases. The esterases, or cells expressing them, are used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Boyce T
Parker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4; Page 12-17; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1713 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                water, meat etc.
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                            AATTGCGCCAACTTTGGTGGCAATCCCGATAATATTACAGTCTTTGGTGAAAGTGCCGGT
                                                                AATGTGCCCGGTAATGCCGGCCTTAAAGATCAAGTCATGGCCTTGCATTGGATTAAAAAT
                                                                                                   ATTAACATACAATATCGTTTGGGAGCTCTAGGTTTTCTAAGTTTAAATTCAGAAGACCTT
                                                                                                                            ATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAAAGCACCCCAGCGACCAACA
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GCTGCCTCTACCCACTACATGATGTTAACCGAACAAACTCGCGGTCTTTTCCATCGTGGT
                                                      AATGTGCCCAGTAATGCCGGCCTTAAAGATCAAGTCATGGCCTTGCGTTGGATTAAAAAT
                                                                                          ATTAACATACAATATCGTTTGGGAGCTCTAGGTTTTCTAAGTTTAAATTCAGAAGACCTT
                   AATTGCGCCAACTTTGGTGGCAATCCCGATAATATTACAGTCTTTGGTGAAAGTGCCGGT
                                                                                                                                                                                                                                                                                                                  AAAGTGAAAGGCGTTAAACGTTTAACTGTGTACGATGATTCCTACTACAGTTTTGAGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       r AG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) COMMONWEALTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        esterase from Lucilia cuprina and related DNA - used to te residues of organo:phosphate and carbamate pesticides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Campbell PM, Newcomb Ri
Robin GC, Russell RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94AU-0003347.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               513 A; 308 C; 368
                                                                                                                                                                                                                                                                                                                                                                                                                                   97.7%;
98.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCI & IND
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1673; DI
Pred. No. 0;
0; Mismatches
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Smyth
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nyth K;
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RESULT

	TCGATGTTTGAAAACATAGAGATTTATTTTAG 1713	1681	Qy
		1681	Db
1680	ATTAGTGATGAATTGAAAATGATTGATGTGCCTGAAATGGATAAGATTAAACAATGGGAG .	1621	Qу
1680		1621	Db
1620 1620	ATGGAAAATGTTTCCTGGGATCCAATTAAGAAATCCGATGAAGTATACAAGTGTTTGAAT	1561 1561	ОУ
1560	ACTGGTATATGGATACAATTTGCCACCACTGGTAATCCTTATAGCAATGAAATTGAAGGT	1501	Qy
1560		1501	Db
1500	AATCAATTGGCCAAACGTATGCCTAAAGAATCGCGTGAATACAAAACAATTGAACGTATG	1441 1441	Qy Db
1440	CGTAGTGGACGTGGTGTAAGGGTGTTAGTCATGCTGATGAATTAACCTATTTCTTCTGG	1381	Qy
1440		1381	Db
1380	GTCTACTTGTATCGCTTCGACTTCGATTCGGAAGATCTTATCAATCCCTATCGTATTATG	1321	Qy
1380		1321	Db
1320	TTCTGGTTCCCCATGCATCGTTTGTTGCAATTACGTTTCAATCACACCTCCGGTACACCC	1261	Qy
1320		1261	Db
1260	CATGTTACAGGAGAAACACCAACAGCTGATAATTTTATGGATCTTTGCTCTCACATCTAT	1201	Qy
1260		1201	Db
1200	GCTGATGCTGAACGCACCGCCCCAGAGACCTTGGAAATGGGTGCTAAAATTAAAAAGGCT	1141 1141	Оy
1140 1140	CAAATGCCTATGCTTGTTAAGGAATTGGAAACTTGTGTCAATTTTGTGCCAAGTGAATTG	1081 1081	Qу
1080	ATACCCACTATGATGGGTAACACTTCATATGAGGGTCTATTTTTCACTTCAATTCTTAAG 	1021 1021	Qу
1020	GCTGATTGTGTCTTACCCAAACATCCTCGGGAAATGGTTAAAACTGCTTGGGGTAATTCG	961	Фр
1020		961	
960	GAAGAGCGTACAAATAAGGTCATGTTTCCTTTTGGTCCCACTGTTGAGCCCATATCAGACC	901 901	ДУ
900	TTTCTTATGAAAGCCAAGCCACAGGATTTAGTAAAACTTGAGGAAAAAGTTTTAACTCTA 	841 841	Оу
840	TTCACCTTAGCCAAATTGGCCGGCTATAAGGGTGAGAATAATGATAAGGATGTTTTGGAA	781	Qy
840		781	Db
780 780	ATACTAATGTCGGGTAATGCTATTTGTCCATTGGCTAATACCCAATGTCAACATCGTGCC	721 721	QУ
720		661	Db

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ID AAQ9
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XX AAQ9
AC AAQ9
XX CP-I
XX Este
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Best Local Similarity
Matches 1687; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                             RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding OP-susceptible esterase E3 of L. cuprina) from a diazinon resistant strain, Llandillo 103. 4 Isolated clones were sequenced (Lc7L103 A-D, AAQ91562-65) that encoded diazinin-resistant esterases. The esterases, or cells expressing them, are used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1713 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         water,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Воусе
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                                                                                                                                                                                                                                                                                                                                                                                                                   bioremediation.
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               TM,
AG,
                                                                                                                                                     AAAGTGAAAGGCGTTAAACGTTTAACTGTGTACGATGATTCCTACTACAGTTTTGAGGGT
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                                                                                                                                                                                                 AAGTTTTTAAACTATCGTTTAACTACCAATGAAACGGTGGTAGCTGAAACTGAATATGGC
                                                                                                                                        AAAGTGAAAGGCGTTAAACGTTTAACTGTGTACGATGATTCCTACTACAGTTTTGAGGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 12-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Campbell PM,
Robin GC, R
                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bioremediation; organophosphate; pesticide; water decontamination;
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1..1713
                                                                                                                                                                                                                                                                                                                                                                                   512 A; 307
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A 1710 bp DNA molecule (AAT68597) comprises the Md-alpha-E7 coding sequence of the Musca domestica Rutgers strain. It was isolated by amplification of genomic DNA using alpha-esterase consensus primers (see also AAT68598-99) and use of a 534 bp amplicon to screen a genomic library of M. domestica. A amplicon of the gene, resulting in substn. of serine for tryptophan at amino acid position 251 (see also AAW17767), confers malathion
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P-PSDB; AAW17767.
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JG, Robin GC,
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Best Local Similarity
Matches 1073; Conserv
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fifth.wipo.int/pub/published_pct_sequences.
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AATGTACCAGGAAATGCTGGCCTCAAGGATCAGGTGCTGGCCCTCAAGTGGATCAAGAAC
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                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from prosophila. The inventiuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG176-ABL30511).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Venter
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical; gene; ss.
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CACAGGATTTAGTAAAACTTGAGGAAAAAGTTTTAACTCTAGAAGAGCGTACAAATAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                             CCCGGTTATGGTTTGGATTCACGGAGGGCTTCATTATCGGCGAGGCCAATCGGGAATG
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                                         TTGGCTACAAGGGCGAGACAACGACAAGGATGTGCTGGAGTTCTTGCAGAACGTAAAGG
                                                        CCGGCTATAAGGGTGAGAATAATGATAAGGATGTTTTTGGAATTTTCTTATGAAAGCCAAGC
                                                                                                                 TTTGTCCATTGGC---TAATACCCAATGTCAACATCGTGCCTTCACCTTAGCCAAATTGG
                                                                                                                                                                    TGTTAACCGAACAACTCGCGGTCTTTTCCATCGTGGTATACTAATGTCGGGTAATGCTA
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                                                                                                TTTGTCCTTGGGCCTACAACGGCGACATTACCCATAATCCCTACAGGATAGCCAAGCTGG
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                                                                                                                                                                                                           TCAAGGATCAGGTGCTGGCCCTCAAGTGGATCAAGAACAATTGCGCTAGTTTCGGCGGAG
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Pred. No. 1.7e-90;
0; Mismatches 615; Indels 263;
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RESULT 12

	4974 AT	Db
	1703 A	Qy
4973	4914 TCGATCTGCCTGAGTGGCCCAAATTGAAGGTCTGGGAGAGCCTCTATGACGACAACAAAG	뫄
1702	1643 TTGATGTGCCTGAAATGGATAAAGATTAAACAATGGGAGTCGATGTTTGAAAAACATAGAG	Qy
4913	4854 CAGTTCGCAAATCCGACGAGGTCATCAAGTGCCTCAACATCAGTGATGACCTGAAGTTCA	Db
1642	1583 CAATTAAGAAATCCGATGAAGTATACAAGTGTTTGAATATTAGTGATTGAAATTGAAATGA	Qy
4853	4794 CTGCCACGGGTAATCCCTACAGCGAGAAGATCAACGGTATGGACACTCTGACCATTGATC	뫄
1582	1523 CCACCACTGGTAATCCTTATAGCAATGAAATTGAAAGTATGGAAAATGTTTCCTGGGATC	Qy
4793	4734 CGAAGGAAAGTCGCGAGTACAGGAACATCGAACGGACCGTGGGCATCTGGACCCAGTTTG	망
1522	1463 CTAAAGAATCGCGTGAATACAAAACAATTGAACGTATGGCTGTATATGGATACAATTTG	Qy
4733	4674 GGGTCAGCCATGCCGACGATTTGAGCTACCAATTCAGCAGCCTGCTGGCTCGCCGGTTGC	рb
1462	1403 GTGTTAGTCATGCTGATGAATTAACCTATTTCTTCTGGAATCAATTGGCCAAACGTATGC	Qy
4673	4614 TCGACTCCGAGGAGCTCATTTTTCCGTACCGCATTATGCGGTTGGGACGCGGTGTCAAGG	Db
1402	1343 TCGATTCGGAAGATCTTATCAATCCCTATCGTATTATGCGTAGTGGACGTGGTGTTAAGG	Qy
4613	4554 TGGTCCATTCCCGACACGCGTACGCGGCTGGAGCTCCAGTATATTTCTATCGATATGACT	망
1342	1283 TGTTGCAATTACGTTTCAATCACACCTCCGGTACACCCCGTCTACTTGTATCGCTTCGACT	Qy
4553	4494 AAGCTGGTAATTTATTTCAGCTCTGTTCGATTTACTACTTCGTGTTTCCGGCCCTGAGGG	Db
1282	1243	Qy
4493	4434 AAGCACCCCAGATAATTACATGGATGTAAGTGTCGTCCAATTAGGTGCTTACATAATCAT	Db
1242	1218 ACCAACAGCTGATAATTTTATGGAT	Qy
4433	4374 TAAAGAAAACTGGATTCGTGGAGTGCACAGATTCGAGATGTTCATCGCACTGGCTCAGA	Дb
1217	1158 CGCCCCAGAGACCTTGGAAATGGGTGCTAAAAATTAAAAAGGCTCATGTTACAGGAGAAAC	Qy
4373	4314 GCAGCAGCTTGATGCTGGCACACCTTTCATTCCCAAAGAATTGCTGGCCACGGAGCCCAG	В
1157	1098 TAAGGAATTGGAAACTTGTGTCAATTTTGTGCCAAGTGAATTGGCTGATGCTGAACGCAC	VΩ
4313	4254 TTCTTTCAATAAGTAAATTTAATTTTATTTCACAGAGGTAAAGCTTATGCCGCAGGTGCT	Дb
1097	1059ATTTTTCACTTCAATTCTTAAGCAAATGCCTATGCTTGT	Qγ
4253	4194 ACACTTCGTACGAGGGCCTGCTGTGGGTTCCAGGTTAGATATTGGGAATTTTTTTGAATT	рь
1058	1040 ACACTTCATATGAGGGTCT	Qy
4193	4134 AGCCTCCAAAGGAGATGAAGACCGCCTGGAGTAACTCCCATCCCCCATGTTTATAGGAA	В
1039		Qy
4133	4074 TAATGTTTGCCTTTGGCCCATCCCTGGAACCATTCTCCACGCCCGAATGTGTGATATCCA	망
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4073	4014 CCAAGGATCTTATTCGCGTGGAGGAAAATGTCCTGACACTGGAGGAACGCATGAACAAGA	ДĎ

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                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 779; 21pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                          (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic
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                        TTGATTTTATAACGGGCAAAGTGTGTGTGGCTCAGAGGATTGTCTATACCTAAAGTGTCTATA
                                                                                                            GACCAACACCCTGGGATGGTGCGTGATTGTTGCAATCATAAAGATAAGTCAGTGCAAG
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           CAAAGAATTTGTATCCCACCAAACCAATGCCCGTGATGGTCTGGATCTATGGCGGTGGCT
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pharmaceutical; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster.
                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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P-PSDB; ABB60586.
                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 8549; 21pp + Sequence Listing; English
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                                                                                                                                                         The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid
genes from Drosophila and
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                                TTAGAGAAACGAGCAGTCTGGAAGGGCAGGATCTACTGGTGCGGCGACTAAAGC---AAC 1280
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                                                               CAAGTGAATTGGCTGATGCTGAACGCACCGCCCCAGAGACCTTGGAAATGGGTGCTAAAA 1189
                                                                                                   AACTAGTAAGAAAAGATCCTTGGGCCTTGAAAAAACTTTCACAACATCCTGCCAAGGGAGG
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 59; 21pp + Sequence Listing; English
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P-PSDB; ABB57756.
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Pred. No. 1.2e-77
0; Mismatches 74
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                                                         TGGAATCAATTGGCCAAACGTATGCCTAAAGAATCGCGTGAATACAAAACAATTGAACGT 1497
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3 Query Match Length DR ID Description	No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution.	25: em_gss_other:* 26: em_gss_pro:* 27: em_gss_rod:*			10: gb_est2:* 11: gb_htc:* 12: gb_est3:* 13: gb_est4:*		en_estnu:* : en_estov:* : em_estpl:*	2: em_estlin;* 3: em_estlin;*	EST	Minimum Match 0% Maximum Match 100% Listing first 45 summaries	length: 0 length: 2000000000	hits satisfying chosen parameters: 32308132	16154066 seqs, 8097743376 residues	IDENTITY_NUC Gapext 1.0	1713 1 atgaatttcaacgttagtttaacatagagatttattttag 1713	April 11, 2003, 00:24:12; Search time 1663.49 Seconds (without alignments) 16677.553 Million cell updates/sec	nucleic search, using sw model	GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
JOURNAL Unpublished (2001) COMMENT Contact: Stapleton, M.	Ephydroidea; Drosophilida Ephydroidea; Drosophilida CE 1 (bases 1 to 778) RS Harvey,D., Brokstein,P., Lewis,S. and Rubin,G.M.	SOURCE fruit fly.  SOURCE fruit fly.  ORGANISM Drosophila melanogaster  Dukaryota; Metazoa; Arthropoda; Hexa	2	RESULT 1 AI062034 AI062034 LOCUS GH01076.5prime GH Drosophila melanocomelanogaster cDNA clone GH01076.5prime GH	ALIGNMENTS	218.6 12.8 609 13 218.6 12.8 611 13 217.8 12.7 612 13	218.6 12.8 609 13 218.6 12.8 609 13 218.6 12.8 609 13	218.6 12.8 588 13 218.6 12.8 607 13	219.8 12.8 614 13 219.2 12.8 615 13 219.6 12.8 587 0	229.2 13.4 622 229.2 13.3 633 222.6 13.0 670	230 13.4 617 13 230 13.4 614 9 229.6 13.4 614 9	230.6 13.5 630 9	231 13.5 638 13	236.2 13.8 656 13 233.2 13.6 628 9	239.2 14.0 056 13 238.4 13.9 656 13 236.8 13.8 656 13	14 243.4 14.2 646 9 AI109901 15 243.4 14.2 646 9 AI293416 16 242.6 14.2 526 9 AI108080 17 241.4 14.1 526 13 AICEGE	246.4 14.4 670 13 245 14.3 648 9 245 14.3 648 9	249.4 14.6 676 13 248.4 14.5 673 13 247 14.4 660 13 246.8 14.4 672 13

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BI1638519 SD20822.5
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BI1637309 RH374350.5
BI1632392 RH54254.5

AI062034
GH01076.5prime GH Drosophila melanogaster head p072 Drosophila melanogaster repaired by the member of the

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18.4 16.4 15.6 15.0 14.9

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AIO62034 AI388926 AI403569 AI517692 BI609541 BI628316

AIJ052034 GH01076.5 AIJ388926 GH19977.5 AIJ38926 GH23036.5 AIJ517692 GH23740.5 BIG09541 RH14337.5 BIG28316 RH56682.5

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AT388926 649 bp mRNA linear EST 19-APR-GH19977.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH19977 5prime similar to U51050: Drosophila melanogaster alpha esterase (aE7) gene, partial cds,
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/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="GH01076"
/clone_lb="GH Drosophila melanogaster head pOT2"
/csex="male and female"
/dev_stage="adult"
/dev_stage="adult"
/lab_host="DH5 - alpha"
/lab_host="DT3"
/note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2: xhoI; Sized fractionated cDNAs were directly ligated int pOT2. Plasmid cDNA library."

pOT2. Plasmid cDNA library."
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                                                                                                                            CGGGCAGTGCCATTTGTCCTTGGGCCTACAACGGCGACATTACCCCATAATCCCTACAGGA
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431 ATCGTGATATGTATGGTCCTGATTATTTCATTAAAAAGGATGTGGTGTTGATTAACATAC 490
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Lewis, S. and Rubin, G.M.
BDGP/HMI Drosophila EST Project
Unpublished (2001)
Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                                                          Email: http://www.fruitfly.org/EST, plate: 199 row: G column: 5
High quality sequence stop: 559.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lawrence Berkeley
One Cyclotron Rd,
Fax: 510 486 6798
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Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster
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AI388926.1
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                                                      Similarity 66.2
21; Conservative
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                                                                                                                                                     165
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                                                                                                                                     /lab_host="DH5 - alpha"
/note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
/note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
XhoI; Sized fractionated cDNAs were directly ligated into
pOT2. Plasmid cDNA library."
160 c 172 g 152 t
                                                                                                                                                                                                                         /clone_lib="GH Drosophila
/sex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
                                                                                                                                                                                                                                                                                                                      /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                      /clone="GH19977"
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                                                                          16.4%;
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Rerkeley, CA
                                                          0;
                                                                          Score 280.8; DB 9;
Pred. No. 2.2e-67;
                                                          Mismatches 212;
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                                                                                            Length
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RESULT 3
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                                                                                                                                                                                                                  Matches
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                                  211
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                                                                                                                                                                                                                                 Local
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                                                          AAAGTGAAAGGCGTTAAACGTTTAACTGTGTACGATGATTCCTACTACAGTTTTGAGGGT 180
                                                                                                             AAGTTTTTAAACTATCGTTTAACCTACCAATGAAACGGTGGTAGCTGAAACTGAATATGGC 120
                                                                                                                                                                                 ATGAATTTCAACGTTAGTTTGATGGAGAAATTAAAATGGAAGATTAAATGCATTGAAAAT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGTTTATAGGAAACACTTCGTACGAGGGCCTGCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTATGATGGGTAACACTTCATATGAGGGTCTATTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTACAAATAAGGTCATGTTTCCTTTTGGTCCCACTGTTGAGCCCATATCAGACCGCTGATT
 ATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCACCCCAGCGACCAACA 240
                                                                                                                                                      ATGAATAAGAACCTCGGCTTTGTGGAGCGCTTGCGGTGGCGCCTCAAAAACCATCGAGCAT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGTGATATCCAAGCCTCCAAAGGAGATGATGAAGACCGCCTGGAGTAACTCCATCCCCA 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCATGAACAAGATAATGTTTGCCTTTGGCCCATCCCTGGAACCATTCTCCACGCCCGAAT 543
                                                                                          AAAGTCCAGCAGTATCGCCAGTCGACCAATGAAACAGTTGTCGCCGACACGGAGTACGGC 210
                                                                                                                                                                                                                  391;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harvey,D., Brokstein,P., Hong,L.,
Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopteryota; Diptera; Brachycera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      One Cyclotron Rd, Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST
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AI403569.1 GI:4246656
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High quality sequence stop: 648.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: http://www.fruitfly.org/EST,
Plate: 230 row: C column: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fruit fly.
                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                             161
                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                      /lab_host="DH5 - alpha"
/note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
XhoI; Sized fractionated cDNAs were directly ligated into
pOT2. Plasmid cDNA library."
174 c 197 g 156 t
                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="GH Drosophila
/sex="male and female"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="GH23036"
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                                                                                                                                                                                                                               15.6%;
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                                                                                                                                                                                                               Score 266.8; DB 9
Pred. No. 1.9e-63,
0; Mismatches 20
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                                                                                                                                                                                                                                             DB 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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Query Match
Best Local Similarity
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ACCESSION
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BDGP/HHMI Drosophila EST Project
Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                   Email: http://www.fruitfly.org/EST, Plate: 287 row: D column: 4 High quality sequence stop: 538.
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Lawrence Berkeley National Lab
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Neoptera; Endopterygota; Diptera; Brachycera;
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/db_xref="taxon:7227"
/db_xref="taxon:7227"
/clone="GH8740"
/clone=lib="GH Drosophila melanogaster head pOT2"
/sex="male and female"
/sex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
/note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
xhoI; Sized fractionated cDNAs were directly ligated into
pOT2. plasmid cDNA library."
170 c 193 g 153 t
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15.0%;
Score 256.6; DB 9 Pred. No. 1.3e-60;
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                   9;
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                 Length 671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Su,C., Tsang,G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pterygota;
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Eukaryota; Metazoa; Arthropoda; Brachycera; Muscomorpha;
Rooptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
Ephydroidea; Drosophilidae; Drosophila.
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1 (Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, J., Champe, M., Guarin, H., Harris, N., Li, P., Liao, G., Misra, S., R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Misra, S., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Misra, Misr
Lawrence Berkeley None Cyclotron Rd, EFax: 510 486 6798 Email: http://www.f
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              est@fruitfly.berkeley.edu
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/dev_stage="Adult"
/lab_host="pH5-alpha TonA"
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/note="Organ: head; Vector: pF1c1; Site_1: XhoI;
/note="Organ: head; Vector: head; Note: head; Not
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/clone="RH14337"
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Pred. No. 5.1e-60;
0; Mismatches 196
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RESULT 5 BI609541 LOCUS

DEFINITION

ACCESSION VERSION KEYWORDS

SOURCE ORGANISM

EST. fruit fly.

REFERENCE AUTHORS

JOURNAL COMMENT

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                                                           ATAACGGGCAAAGTGTGTGTGGCTCAGAGGATTGTCTATACCTAAGTGTCTATACGAATAAT
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                                                                                                          GTCTTCGATAAGGTAGAGGGCTCCGAGGACTGCCTCTATCTCAATGTGTACACCAACAAT
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367; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: http://www.fruitfly.org/EST, Plate: RH.566 row: G column: 10 High quality sequence stop: 558. Location/Qualifiers
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One Cyclotron Rd, Berkeley,
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Contact: Stapleton, M.
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Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 674)
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/Sex="male and female"
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/Gev_stage="Adult"
/lab_host="DH5-alpha TonA"
/lab_host="DH5-alpha TonA"
/note="Organ: head; Vector: pFlc1; Site_1: XhoI; Site_2:
BamHI; Library was kindly generated by Piero Carninci at
the RIKEN. The library was normalized and excised using
Cre recombinase. Plasmid CDNA library."
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/db_xref="taxon:7227"
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Pred. No. 9.3e-59;
0; Mismatches 196;
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ATACCGTACGCCCAACCGCCAGTGGGTGAGCTTGAGATTTAAAGCACCCCAGCGACCAACA
                                                  CAAGTGAGGGGTATCAAGCGTCTATCTCTACGATGTGCCCTACTTCAGCTTCGAGGGT
                                                                                 AAAGTGAAAGGCGTTAAACGTTTAACTGTGTACGATGATTCCTACTACAGTTTTGAGGGT
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B16705.5prime SD Drosophila melanogaster Schneider L2 cell culture port2 brosophila melanogaster cDNA clone SD16705 5 similar to alpha-Est7: FBan0001112 GO:[carboxyesterase (GO:0004091); carboxyesterase (GO:0004091)] located on: 3R 84D5-84D5;: 05/18/2001
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BDGP/HHMI Drosophila EST Project
Unpublished (2001)
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Meoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophillae; Drosophila.
1 (bases 1 to 676)
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One Cyclotron Rd, Berkeley, CA 94720, USA
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                                                                                                                                                                                                                                                                                                                                       Plasmid cDNA library.
173 c 194 g
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fractionated cDNAs were directly ligated int
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/db_xref="taxon:7227"
/clone="SD16705"
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0; Mismatches 196;
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                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 673)
Stapleton,M., Brokstein,P., Hong,L., Tyler,D., Berman,B., Carlson Stapleton,M., Brokstein,P., Hong,L., Tyler,D., Frise,E., George,J., Champe,M., Chavez,C., Dorsett,V., Farfan,D., Frise,E., George,R., Gonzalez,M., Guarin,H., Harris,N., Li.P., Liao,G., Misra,S., Mungall,C.J., Nunoo,J., Pacleb,J., Paragas,V., Park,S., phouanenavong,S., Wan,K., Yu,C., Lewis,S.E., Celniker,S. and Rubin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                         BDGP/HHMI RH Drosophila EST Project
Unpublished (2001)
Contact: Stapleton, M.
                                                                                                                                                                                                                                 Email: http://www.fruitfly.org/EST/
plate: RH.434 row: H column: 9
High quality sequence stop: 553.
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One Cyclotron Rd, Berkeley, CA 94720,
Fax: 510 486 6798
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     /note="Organ: head; Vector: pFlc1; Site_1: xhoI; Site_2: BamHI; Library was kindly generated by Piero Carnincl at the RIKEN. The library was normalized and excised using the RIKEN.
                                                                                                                                               /organism="Drosophila
/db_xref="taxon:7227"
/clone="RH43493"
                                                        /sex="male and female"
/dev_stage="Adult"
/lab_host="DH5-alpha TonA"
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                                                   Harvey,D., Brokstein,P.,
Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST
Unpublished (2001)
                                                                                                    Eukaryota, Metazoa; Arthropoda; mexapoda; Neoptera; Endopteryyota; Diptera; Brachycera; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 660)

1 (bases 1 to 660)
                                                                                                                                                Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda;
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Lawrence Berkeley National One Cyclotron Rd, Berkeley,
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Email: http://www.fruitfly.org/EST,
Plate: SD.220 row: F column: 7
High quality sequence stop: 546.
BIG114443 672 bp mRNA linear EST 07-SEP-2001 RH43812.5prime RH Drosophila melanogaster normalized Head pFlc-1 Drosophila melanogaster cDNA clone RH43812 5 similar to alpha-Est7: FBan0001112 GO:[carboxyesterase (GO:0004091); carboxyesterase
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/lab_host="DH5-alpha"
/note="Vector: pOT2; Site_1: EcoRI; Site_2: fractionated cDNAs were directly ligated int plasmid cDNA library."
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/db_xref="taxon:7227"
/clone="SD22067"
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 672)
Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Car
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: http://www.fruitfly.org/EST, Plate: RH.438 row: A column: 12 High quality sequence srop: 554. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Misra, S., Mungall, C.J., Nunco, J., Pacleb, J., Paragas, V., Park, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  One Cyclotron Rd, Fax: 510 486 6798
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One Cyclotron Rd, Berkeley, CA
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/lab_host="DH5-alpha Tona"
/lab_host="DH5-alpha Tona"
/note="Organ: head; Vector: pFlc1; Site_1: XhoI; Site_2:
/note="Organ: head; Vector: pFlc1; Site_1: XhoI; Site_2:
/note="Organ: head; Vector: pFlc1; Site_1: XhoI; Site_2:
/note="Organ: head; Vector: pFlc2; Site_1: XhoI; Site_2:
/note="Organ: head; Vector: pFlc1; Site_1: XhoI; Site_2: XhoI; Sit
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pFlc-1"
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/db_xref="taxon:7227"
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Pred. No. 7.3e-58;
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AAGTTTTTAAACTATCGTTTAACTACCAATGAAACGGTGGTAGCTGAAACTGAATATGGC
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                                                    ATGAATAAGAACCTCGGCTTTGTGGAGCGCTTGCGGTGGCGCCTCAAAACCATCGAGCAT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 670)
Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Misra, S., Mungall, C.J., Nunco, J., Pacleb, J., Paragas, V., Park, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BIC33302 670 bp mRNA linear EST RE29491. Sprime RE Drosophila melanogaster normalized Emb Drosophila melanogaster cDNA clone RE29491 5 similar to FBan0001112 located on: 3R 84D5-84D5;: 04/12/2001, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: http://www.fruitfly.org/EST, Plate: RE.294 row: H column: 7 High quality sequence stop: 534.
Location/Qualifiers
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Lawrence Berkeley National Lab
Lawrence Berkeley, CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BDGP/HHMI RE Drosophila Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phouanenavong,S., Wan,K., Yu,C., Lewis,S.E., Celniker,S. and Rubin
                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cyclotron Rd, : 510 486 6798
                                                                                                                                                                                                                152
                                                                                                                         Conservative
                                                                                                                                                                                                          /note-"Organ: embryo; Vector: pF1c1; Site_1: XhoI; Site_2: BamHI; Library was kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library."

168 c 194 g 155 t l others
                                                                                                                                                                                                                                                                                                                                                                                   /organism="prosophila melanogaster"
/db_xref="taxon:7227"
/clone="RE29491"
                                                                                                                                                                                                                                                                                               /sex="male and female"
/dev_stage="0-24 hours mixed stage
/lab_host="DH5-alpha TonA"
                                                                                                                                                                                                                                                                                                                                                               /clone_lib="RE Drosophila melanogaster normalized
                                                                                                                                         14.4%;
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 648)
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                                                                                                                                                                                                                                              One Cyclotron Rd, Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
AII13763
AII13763.1 GI:3514566
                                                                                                                                                                  Email: http://www.fruitfly.org/EST, plate: 102 row: B column: 1
High quality sequence stop: 435.
Location/Qualifiers
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One Cyclotron Rd, Berkeley, CA
                                                                                                                                                                                                                                                                                                                        Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                          Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                 Harvey,D., Brokstein,P.,
               /clone_lib="GH Drosophila
/sex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
                                                                                         /organism="Drosophila
/db_xref="taxon:7227"
/clone="GH10213"
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por2;
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   ECORI;
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362; Conservative
                                                                                       Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 648)
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Drosophila melanogaster alpha esterase (aE7) gene, partial cds.
                                        BDGP/HHMI Drosophila EST Unpublished (2001)
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                                                                 Harvey, D., Brokstein, P., Hong, L., Lewis, S. and Rubin, G.M.
Lawrence Berkeley National Lab
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Email: http://www.fruitfly.org/EST,
Plate: 224 row: F column: 4
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/sex="male and female"
/dev_stage="adult"
/lab_host="DH5" alpha"
/note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_1
XhoI; Sized fractionated cDNAs were directly ligated in pOT2. Plasmid cDNA library."
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Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 646)
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One Cyclotron Rd, Berkeley, CA 9472(
Fax: 510 486 6798 fruitfly.org/EST,
Email: http://www.fruitfly.org/EST,
Plate: 92 row: H column: 8
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Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
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ATTAACATACAATATCGTTTGGGAGCTCTAGGTTTTCTAAGTTTAAATTCAGAAGACCTT
                                                                         GGTGAAAATCATCGTGATATGTATGGTCCTGATTATTATAAAAAAGGATGTGGTGTTG
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/db_xref="taxon:7227"
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Reoptera; Endopterygora; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
Ephydroidea; Drosophilidae; Drosophila.
In (bases 1 to 646)
Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M
Lewis,S. and Rubin,G.M.
Lewis,S. and Rubin,G.M.
EphylHMI Drosophila EST Project
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                                                      ATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCACCCCAGCGACCAACA 240
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plate: 65 row: B column: 12
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Location/Qualifiers
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Fax: 510 486 6798
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One Cyclotron Rd, Berkeley, CA
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/clone_lib="LP Drosophila melanogas
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TITLE OF INVENTION: MALATHION CARBOXYLESTERASE
FILE REFERENCE: Attorney Docket No. 623515 50179
CURRENT APPLICATION NUMBER: US/09/068,960A
CURRENT FILING DATE: 1996-05-20
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER FILING DATE: 1996-11-22
EARLIER FILING DATE: 1995-11-23
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 1713
TYPE: DNA
ORGANISM: Lucilia cuprina
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...; ORGANISM: Lucilia c
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TITLE OF INVENTION: MALATHION CARBOXYLESTERASE
FILE REFERENCE: Attorney Docket No. 62355.5 50179-051
CURRENT APPLICATION NUMBER: US/09/068,960A
CURRENT FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER FILING DATE: 1996-11-22
EARLIER APPLICATION NUMBER: AU 6751
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FILE REFERENCE: Attorney Docket No. 6235515 50179-051
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FILE REFERENCE: Attorney Docket No. 6235515 50179-051
FILE REPLICATION NUMBER: US/09/068,960A
CURRENT FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER APPLICATION NUMBER: AU 6751
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1713 base pair
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APPLICANT:
TITLE OF IN
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                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
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                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                NAME: Price, Robert L. REGISTRATION NUMBER: 2
                                                                                                                                                   Local Similarity
nes 1704; Conser
                                                                                                                                                                                                                                                  TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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PARKER, Anthony G.
OAKESHOTT, John G.
SMYTH, Kerrie A.
NVENTION:
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BOYCE, Thomas M
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                          GCTGATGCTGAACGCACCGCCCCAGAGACCTTGGAAATGGGTGCTAAAATTAAAAAGGCT
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APPLICANN: Commonwealth Scientific and Industrial Rsrch. Org
TITLE OF INVENTION: MALATHION CARBOXYLESTERASE
FILE REFERENCE: Attorney Docket No. 6235515 50179-051
CURRENT APPLICATION NUMBER: US/09/068,960A
CURRENT FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER APPLICATION NUMBER: AU 6751
EARLIER APPLICATION NUMBER: AU 6751
EARLIER FILING DATE: 1996-11-23
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 1713
TYPE: DNA
ORGANISM: Lucilia cuprina
US-09-068-960-7
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Patent No. 6235515
GENERAL INFORMATION:
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Best Local Similarity 99.
Matches 1704; Conservative
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                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/669,524
FILING DATE:
CLASSIFICATION: 435
ATTORNEX/AGENT INFORMATION:
NAME: Price, Robert L.
REGISTRATION UMBER: 22,685
REFERENCE/DOCKET NUMBER: 1451-021
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELECOMMUNICATION INFORMATION:
                                                 TELEFAX: 703-684-1124 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: RUSSELL, Robyn J.
APPLICANT: NEWCOMB, Richard
APPLICANT: ROBIN, Geoffrey C
APPLICANT: BOYCE, Thomas M.
APPLICANT: CAMPELL, Petter
APPLICANT: PARKER, Anthony G
APPLICANT: OAKESHOTT, John G
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                         SEQUENCE CHARACTERISTICS:
LENGTH: 1713 base pairs
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ADDRESSEE: Lowe Price
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                                                                                                                                                                                                                                                                         STREET: 99 Canal CITY: Alexandria STATE: Virginia COUNTRY: USA ZIP: 22314
                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
LENGTH: 1713 bi
TYPE: nucleic a
STRANDEDNESS: s
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BOYCE, Thomas M.
CAMPELL, Peter M.
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                     GAAGAGCGTACAAATAAGGTCATGTTTCCTTTTGGTCCCACTGTTGAGCCATATCAGACC
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RESULT 8
US-09-068-960-14
) Sequence 14, Application US/09068960A
patent No. 6235515

GENERAL INFORMATION:
APPLICANT: COMMONWEALTH SCIENTIFIC and Industrial Rsrch.
FILE REFERENCE: Attorney Docket No. 6235515 50179-051
CURRENT APPLICATION NUMBER: US/09/068,960A
CURRENT FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER APPLICATION NUMBER: BCT/AU96/00746
EARLIER APPLICATION NUMBER: DCT/AU96/00746
EARLIER APPLICATION NUMBER: DCT/AU96/00746
SEARLIER APPLICATION NUMBER: DCT/AU96/00746
EARLIER APPLICATION NUMBER: DCT/AU96/00746
SEARLIER FILING DATE: 1996-11-22
EARLIER APPLICATION NUMBER: DCT/AU96/00746
SEQ ID NO 14
LENGTH: 1710
TYPE: DNA
ORGANISM: Musca domestica
US-09-068-960-14
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                                               TTGAGCCATATCAGACCGCTGATTGTGTCTTACCCAAACATCCTCGGGAAATGGTTAAAA 1003
                                                                                             AAAAAGTTTTAACTCTAGAAGAGCGTACAAATAAGGTCATGTTTCCTTTTGGTCCCACTG
                                                                                                                            ATAAGGATGTTTTGGAATTTCTTATGAAAGCCAAGGCACAGGATTTAGTAAAACTTGAGG
                                                                                                                                                                                                                                                                                    TGCATTGGATTAAAAATTAGTGCGCCAACTTTGGTGGCAATCCCGATAATATTACAGTCT
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                                                                           CACAAGTTTTGACACCCGAAAGAATGCAAAATAAGGTCATGTTTCCTTTTGGACCCACTG
                                                                                                                  AAAAAGATATCCTGGAATTCCTAATGAAAGCCAATCCCTATGATTTGATCAAAGAGGAGC
                                                                                                                                                        AATGCCAAAGTCGTGCGCTCACCATGGCCAAACGTGTTGGCTATAAGGGAGGAGGACAATG
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73.2%;
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Pred. No. 1.3e-264;
O; Mismatches 447;
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	AAATTAAACAATGGGCAAGTATATTCGATAAAAAGGAAGG	1664	Дb
		1664	Qy
1663	TCTATAAATGTTTAAATATCGGCGATGAATTGAAAGTTATGGATTTGCCAGAAATGGATA	1604	DЬ
1663	TATACAAGTGTTTGAATATTAGTGATGAATGAATGAATGA	1604	Qy
1603	GCAATGATATAGCCGGCATGGAAAACCTCACCTGGGATCCCATAAAAAAAA	1544	Db
1603	GCAATGAAATTGAAGGTATGGAAAATGTTTCCTGGGATCCAATTAAGAAATCCGATGAAG	1544	Qy
1543	AAACCATTGAACGCATGGGTTGGCATTTGGACGGAATTCGCCACCACCACCAAAACCATACA	1484	Db
1543	AAACAATTGAACGTATGACTGGTATATGGATACAATTTGCCACTGGTAATCCTTATA	1484	Qy
1483	TAACCTATCTCTTCTGGAACATTTTGTCGAAACGCCTGCCAAAGGAAAGCCGCGAATACA	1424	Db
1483	TAACCTATTTCTTCTGGAATCAATTGGCCAAACGTATGCCTAAAGAATCGCGTGAATACA	1424	Qy
1423	ACCCCTATCGTATTATGCGTTTTGGCCGTGGCGTTAAAGGTGTAAGCCATGCCGATGAGC	1364	Db
1423	ATCCCTATCGTATTATGCGTAGTGGACGTGGTGTTAAGGGTGTTAGTCATGCTGATGAAT	1364	Qy
1363	ACACAGCTGGCACTCCCATTTATTTGTATCGTTTCGATTTCGATTCCGAAGAAATTATTA	1304	Ъ
1363	ACACCTCCGGTACACCCGTCTACTTGTATCGCTTCGACTTCGATTCGGATGCTTATCA	1304	Qy
1303	TTTGCTCCTATTTCTATTTCCTCTTCCCCATGCATCGCTTCCTACAATTGCGCTTCAACC	1244	В
1303	TTTGCTCTCACATCTATTTCTGGTTCCCCCATGCATCGTTTGTTGCAATTACGTTTCAATC	1244	Qy
1243	CCATTGTGAAAAAGGCCCATGTGGATGGGGAAACACCTACTCTGGATAATTTTATGGAGC	1184	Db
1243	CTAAAATTAAAAAAGGCTCATGTTACAGGAGAAACACCCAACAGCTGATAATTTTATGGATC	1184	Qy
1183	ATGTGCCTTGGGAGTTGACAGTGAACGCAGTGCCCCGGAAACCCTGGAGAGGGCTG	1124	DЬ
1183	TTGTGCCAAGTGAATTGGCTGATGCTGAACGCACCGCCCCAGAGACCTTGGAAATGGGTG	1124	Qy
1123	CCAAATCAATTGCCAAACAATATCCGGAGGTTGTAAAAGAGTTGGAATCCTGTGTGAATT	1064	Db
1123	TCACTTCAATTCTTAAGCAAATGCCTATGCTTGTTTAAGGAAATTGGAAACTTGTGTCAATT	1064	Qy

US-08-747-221B-51

Sequence 51, Application US/08747221B

Sequence 51, Application US/08747221B

Patent No. 6063610

GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Wisnewski, Nancy
TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic.
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof

RUMBER OF SEQUENCES: 66

CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION NUMBER: US/08/747,221B
FILING DATE: No. 6063610ember 12, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

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RESULT 10
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US-08-747-2218-51
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Sequence 52, Application US/08747221B Patent No. 6063610 GENERAL INFORMATION:
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Best Local Similarity 56:4%;
Matches 361; Conservative
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INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 1544 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Verser, Carol Talkington REGISTATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970,493-7272
TELEPHONE: 970,493-7272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89 CTGGAATTCCATATGCCAAACCTCCTGTAGGTGATCTAAGATTTAAGCCACCTCAACCTG
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STRANDEDNESS: single
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                                                                                                                        AAGCGATCTCACAAAGTGGAAGTGCTTTTAATCCTTGGGC
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                                                                                                                                                      GTGGTATACTAATGTCGGGTAATGCTATTTGTCCATTGGC
                                                                                                                                                                                      CAGGTGGTGCAAGTGTTCATTATTTGATGTTATCAGATCTTTCCAAAGGACTTTTTCATA
                                                                                                                                                                                                                                                           AAAACAATATTGCATCCTTTGGTGGTGACCCCAACAATGTGACTATTTTTGGAGAATCAG
                                                                                                                                                                                                                                                                               AAAATAATTGCGCCAACTTTGGTGGCAATCCCGATAATATTACAGTCTTTGGTGAAAGTG
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                                                                                                                                                                                                                                                                                                                              AA-----GCGCCTGGCAATGTTGGTTTGATGGACCAGGTTGAAGCTCTAAAATGGGTAA
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Pred. No. 1.7e-42;
0; Mismatches 273;
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APPLICANT:

Silver,

Gary

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Best Local Similarity 56.4%;
Matches 361; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Verser, Carol Talkington REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
                                                                                                                                                                      1256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: NO. 6063610el Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1584 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                     1316 CAAAAACATCAGAGAAATCACTTCTTCCAGTAATGGTATGGATACATGGAGGAGGCTTCT 1257
                                                                                                                                                                                                                                                                                                                                                                                                                           1436 CAGAACCTTGGTCAGGTGTTCTTGATGCTAGTAAAGAAGGGAATAGTTGTAGATCAGTAC 1377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1556 AAGGTACTTTAAAAGGAAAAGAGCAAATTAGTGAAAAAGGAAATGTGTTCCATAGTTATT 1497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                               TGTTGATTAACATACAATATCGTTTGGGAGCTCTAGGTTTTCTAAAGTTTAAATTCAGAAG
AA-----GCGCCTGGCAATGTTGGTTTGATGGACCAGGTTGAAGCTCTAAAATGGGTAA
                                   ACCTTAATGTGCCCGGTAATGCCGGCCTTAAAGATCAAGTCATGGCCTTGCATTGGATTA
                                                                                 TTCTGGTTACTTTCAATTATCGATTAGGTGTTTTTGGGATTTTTGAACCTGGGAATAGAAG
                                                                                                                                                                                                                                                                              ATTTTATAACGGGCAAAGTGTGTGGCTCAGAGGATTGTCTATACCTAAGTGTCTATACGA 355
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                                                                                                                                                                                                                                                                                                                                            ATTTTATTAAAAAAATTAAAGTAGGGGCTGAAGATTGTTTATACCTCAATGTCTATGTAC 1317
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Pred. No. 1.7e-42;
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RESULT 11
US-09-005-051-51
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                                                                                                                                              Query Match 10.6%;
Best Local Similarity 56.4%;
Matches 361; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Silver, Ga
APPLICANT: Wisnewski,
                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: FC TELECOMMUNICATION INFORMATION: 970/493-7272
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                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1584 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/747,221 FILING DATE: No. 6291222ember 12, ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: WordPerfect for Windows, Version 7.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1082 AAAACAATATTGCATCCTTTGGTGGTGACCCCAACAATGTGACTATTTTTGGAGAATCAG 1023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 9:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Verser, Carol Talkington REGISTRATION NUMBER: 37,459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                       TOPOLOGY: 1ir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
CTGGAATTCCATATGCCAAACCTCCTGTAGGTGATCTAAGATTTAAGCCACCTCAACCTG 148
                 AGGGTATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCACCCCAGCGAC 235
                                                                                                         ATGGCAAAGTGAAAGGCGTTAAACGTTTAACTGTGTACGATGATTCCTACTACAGTTTTG 175
                                                                      AAGGTACTTTAAAAGGAAAAGAGCAAATTAGTGAAAAAGGAAATGTGTTCCATAGTTATT 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37,459
                                                                                                                                                                                                                                                                                                                                                                                                                 51:
                                                                                                                                              Score 181.2; DB 4; Pred. No. 1.7e-42; 0; Mismatches 273;
                                                                                                                                                                                 DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        923
                                                                                                                                                                                   Length 1584;
                                                                                                                                                Indels 6;
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US-09-005-051-52/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 6291222
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                    SOFTWARE: WordPerfect for Windows, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                  APPLICATION NUMBER: 08/747,221
FILING DATE: No. 6291222ember 12,
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NO. 6291222el Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Silver, Gary W. APPLICANT: Wisnewski, Nanc
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                 REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC
                               NAME: Verser, Carol Talkington REGISTRATION NUMBER: 37,459
                                                                                                                                                                                                                                                                                                                                                                        STREET: 1825 Sharp Point Drive CITY: Fort Collins
                                                                                                                                                               FILING DATE:
                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                       OPERATING SYSTEM: Windows
                                                                                                                                                                                                                                                                 COMPUTER:
                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Carol Talkington Verser, Ph.D. ADDRESSEE: Heska Corporation
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291222
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TELEPAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 1584 nucleotides
TYPE: nucleic acid
companymenumes:
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                                                                                                                                                                     RESULT 13
US-08-747-2218-36
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                                                                                                                                    Sequence 36, Application US/08747221B Patent No. 6063610
                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176 AGGGTATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCACCCCAGCGAC
                          APPLICANT: Silver, Gary W.
APPLICANT: Wisnewski, Nancy
TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   236
                                                                                                                                                                                                                               962 AAGCGATCTCACAAAGTGGAAGTGCTTTTAATCCTTGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 10.6%; Local Similarity 56.4%;
ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAACACCCTGGGATGGTGTGCGTGATTGTTGCAATCATAAAGATAAGTCAGTGCCAACTTG 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATICGETGAAAATCATCGTGATATGTATGGTCCTGATTATTTCATTAAAAAGGATGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTCTGGTTACTTCAATTATCGATTAGGTGTTTTGGGATTTTTGAACCTGGGAATAGAAG 1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTTTATTAAAAAAATTAAAGTAGGGGCTGAAGATTGTTTATACCTCAATGTCTATGTAC 1317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTTATAACGGGCAAAGTGTGTGGCTCAGAGGATTGTCTATACCTAAGTGTCTATACGA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGTTGATTAACATATCAGAAGGTTTGGGAGGTTTTCTAAGTTTAAATTCAGAAG 535
                                                                                                                                                                                                                                                                GTGGTATACTAATGTCGGGTAATGCTATTTGTCCATTGGC
                                                                                                                                                                                                                                                                                               CAGGTGGTGCAAGTGTTCATTATTTGATGTTATCAGATCTTTCCAAAGGACTTTTTCATA 963
                                                                                                                                                                                                                                                                                                                 CCGGTGCTGCCTCTACCCACCTACATGATGTTAACCGAACAAACTCGCGGGTCTTTTCCATC 715
                                                                                                                                                                                                                                                                                                                                                            AAAACAATATTGCATCCTTTGGTGGTGACCCCAACAATGTGACTATTTTTGGAGAATCAG
                                                                                                                                                                                                                                                                                                                                                                               AAAATAATTGCGCCAACTTTGGTGGCAATCCCGATAATATTACAGTCTTTGGTGAAAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                     AA-----GCGCCTGGCAATGTTGGTTTGATGGACCAGGTTGAAGCTCTAAAATGGGTAA 1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCTTAATGTGCCCGGTAATGCCGGCCTTAAAGATCAAGTCATGCCTTGCCATTGGATTA 595
 Carol Talkington Verser, Heska Corporation
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Pred. No. 1.7e-4;
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Best Local
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Ve
SOFTWARE: WordPerfect for Windows, Ve
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/747,221B
FILING DATE: No. 6063610ember 12, 19;
CLASSIETCATION: 435
CLASSIETCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION UNUMBER: 37,459
REGISTRATION UNUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2007 nucleotid
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1825 Sha:
CITY: Fort Collii
STATE: Colorado
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                              39 AAGGTACTTTAAAAGGAAAAGAGCAAATTAGTGAAAAAGGAAATGTGTTCCATAGTTATT 98
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LOCATION:
513
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                                                                                                                                                                                                                                                                                                             ATTTTATAACGGGCAAAGTGTTGTGTGCTCAGAGGATTGTCTATACCTAAGTGTCTATACGA 355
                                                                                                                                                                                                                                                                                                                                                     CAGAACCTTGGTCAGGTGTTCTTGATGCTAGTAAAGAAGGGAATAGTTGTAGATCAGTAC 218
                                                                                                                                                                                                                                                                                                                                                                     CAACACCCTGGGATGGTGTGGTGATTGTTGCAATCATAAAGATAAGTCAGTGCAAGTTG 295
                                                                                                                                                                                           TTATCGGTGAAAATCATCGTGATATGTATGGTCCTGATTATTTCATTAAAAAAGGATGTGG 475
                                                                                                                                                                                                                                                      TCATGGGATCTGGAAATAGTGATATGTATGGTCCTGAATATTTGATGGATTATGGAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361;
AAAATAATTGCGCCAACTTTGGTGGCAATCCCCGATAATATTACAGTCTTTGGTGAAAGTG 655
                                                        AA-----GCGCCTGGCAATGTTGGTTTGATGGACCAGGTTGAAGCTCTAAAATGGGTAA
                                                                                  ACCTTAATGTGCCCGGTAATGCCGGCCTTAAAGATCAAGTCATGGCCTTGCATTGGATTA 595
                                                                                                                 TTCTGGTTACTTTCAATTATCGATTAGGTGTTTTGGGGATTTTTGAACCTGGGAATAGAAG
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Pred. No. 1.9e-42;
0; Mismatches 273;
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                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 361; Conserv
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GENERAL INFORMATION:
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                                        1789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 2007 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Verser, Carol Talkington REGISTRATION NUMBER: 37,459 REFERENCE/DOCKET NUMBER: FC-1 TELECOMMUNICATION INFORMATION: TELEPHONE: 970/493-7272 TELEFAX: 970/484-9505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                         1969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: Windows 95 SOFTWARE: Worlderfect for Windows, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NO. 6063610el Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
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APPLICANT: Wisnewski,
                                                                                                                                                                                            1909
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  356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: No. 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Carol Talkington Verser, Ph.D. ADDRESSEE: Heska Corporation STREET: 1825 Sharp Point Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                     ATGGCAAAGTGAAAGGCGTTAAACGTTTAACTGTGTACGATGATTCCTACTACAGTTTTG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCGGTGCTGCCTCTACCCACTACATGATGTTAACCGAACAACTCGCGGTCTTTTCCATC 715
                                                                                                                                     CAACACCCTGGGATGGTGCGTGATTGTTGCAATCATAAAGATAAGTCAGTGCAAGTTG
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CTGGAATTCCATATGCCAAACCTCCTGTAGGTGATCTAAGATTTAAGCCACCTCAACCTG 1850
                                                                                                                                                                                                                                AGGGTATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCACCCCCAGCGAC 235
                                                                                                                                                                                                                                                                     AAGGTACTTTAAAAAGGAAAAAGAGCAAATTAGTGAAAAAGGAAATGTGTTCCATAGTTATT 1910
                                      ATTTTATTAAAAAAATTAAAGTAGGGGGCTGAAGATTGTTTATACCTCAATGTCTATGTAC
                                                                        ATTTTATAACGGGCAAAGTGTGTGGCTCAGAGGATTGTCTATACCTAAGTGTCTATACGA 355
                                                                                                               CAGAACCTTGGTCAGGTGTTCTTGATGCTAGTAAAGAAGGGAATAGTTGTAGATCAGTAC
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o. 606361(
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ki, Nancy
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6063610ember 12,
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Pred. No. 1.9e-42;
0; Mismatches 273;
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US-09-005-051-36
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                                                                                                                                           CLASSIFICATION DATA:

PRIOR APPLICATION NUMBER: 08/747,221

APPLICATION NUMBER: 08/747,221

FILING DATE: NO. 629122ember 12, 19

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: FC-1

TELEPHONE: 970/493-7272

TELEPHONE: 970/493-7272

TELEPAX: 970/493-7272
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                                                                                                                                 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 2007 nucleotides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid
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                    MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  416 TTATCGGTGAAAATCATCGTGATATGTATGGTCCTGATTATTTCATTAAAAAGGATGTGG
                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Carol Talkington Verser,
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
                                      TOPOLOGY:
                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGCGATCTCACAAAGTGGAAGTGCTTTTAATCCTTGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGGTATACTAATGTCGGGTAATGCCTATTTGTCCATTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGGTGGTGCAAGTGTTCATTATTTGATGTTATCAGATCTTTCCAAAGGACTTTTTCATA 1376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCGGTGCTGCCTCTACCCCACTACATGATGTTAACCGAACAAACTCGCGGTCTTTTCCATC 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAACAATATTGCATCCTTTGGTGGTGACCCCAACAATGTGACTATTTTTGGAGAATCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAATAATTGCGCCAACTTTGGTGGCAATCCCCGATAATATTACAGTCTTTGGTGAAAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA-----GCGCCTGGCAATGTTTGGTTTGATGGACCAGGTTGAAAGCTCTAAAAATGGGTAA 1496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCTTAATGTGCCCGGTAATGCCGGCCTTAAAGATCAAGTCATGGCCTTGCATTGGATTA 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTCTGGTTACTTTCAATTATCGATTAGGTGTTTTTGGGATTTTTGAACCTGGGAATAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGTTGATTAACATACAATATCGTTTGGGAGCTCTAGGTTTTCTAAGTTTAAATTCAGAAG
                                                                      nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Colorado
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IBM PC compatible
---- windows 95
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LOCATION:
US-09-005-051-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 10.6%; Score 181.2; DB 4; Length 2007; Best Local Similarity 56.4%; Pred. No. 1.9e-42; Matches 361; Conservative 0; Mismatches 273; Indels 6; Gaps
                                      716 GTGGTATACTAATGTCGGGTAATGCTATTTGTCCATTGGC 755
                                                                                                                                    459
                                                                                596 AAAATAATTGCGCCAACTTTGGTGGCAATCCCGATAATATTACAGTCTTTGGTGAAAGTG 655
                                                                                                                                           536 ACCTTAATGTGCCCGGTAATGCCGGCCTTAAAGATCAAGTCATGGCCTTGCATTGGATTA 595
                                                                                                                                                                    339 TCATGGGATCTGGAAATAGTGATATGTATGGTCCTGAATATTTGATGGATTATGGAATTG 398
                                                                                                                                                                                                                            416 TTATCGGTGAAAATCATCGTGATATGTATGGTCCTGATTATTTCATTAAAAAGGATGTGG 475
                                                                                                                                                                                                                                                      116 ATGGCAAAGTGAAAGGCGTTAAACGTTTAACTGTGTGTACGATGATTCCTACTACAGTTTTG 175
                                                                                                                                                                                                                                                                                                  219 ATTITATTAAAAAAATTAAAGTAGGGGCTGAAGATTGTTTATACCTCAATGTCTATGTAC 278
                                                                                                                                                                                                                                                                                                              296 ATTTTATAACGGGCAAAGTGTGTGGCTCAGAGGAGTTGTCTATACCTAAGTGTCTATACGA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                 39 AAGGTACTTTAAAAGGAAAAGAGCAAATTAGTGAAAAAGGAAATGTGTTCCATAGTTATT 98
AAGCGATCTCACAAAGTGGAAGTGCTTTTAATCCTTGGGC 672
                                                                                                                          AA-----GCGCCTGGCAATGTTGGTTTGATGGACCAGGTTGAAGCTCTAAAATGGGTAA 512
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Search completed: April 11, 2003, 08:51:22 Job time: 46.5118 secs

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Perfect score:
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq length: 0 seq length: 2000000000
Published_Applications_Na:*

1: /cgn2_6/ptodata/2/pubpna/vg
2: /cgn2_6/ptodata/2/pubpna/vg
3: /cgn2_6/ptodata/2/pubpna/vg
3: /cgn2_6/ptodata/2/pubpna/vg
4: /cgn2_6/ptodata/2/pubpna/vg
6: /cgn2_6/ptodata/2/pubpna/vg
6: /cgn2_6/ptodata/2/pubpna/vg
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13: /cgn2_6/ptodata/2/pubpna/vg
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1713
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Listing first 45 summaries
/cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
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                                                                                                                                                                                                                                                                                                                                                                     /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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15895.765 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Result No.	Score	Query Match	Length	DB	ID	Description
1	87.2	5.1	1691	ِ و	US-10-083-590-13	Sequence 13, Appl
N	78.8	4.6	1611	9	US-09-738-626-1254	1254
w	63.8	3.7	1967	10	US-09-748-739A-1	
4	63.8	3.7	2381	10	US-09-880-107-2271	Sequence 2271, Ap
υī	63.8	3.7	2416	10	US-09-748-739A-3	Sequence 3, Appli
6	63.8	3.7	2416	10	US-09-748-739A-5	Sequence 5, Appli
7	63.8		2416	10	US-09-748-739A-7	7,
80	63.8	3.7	2416	10	US-09-748-739A-16	σ
9	63.8		2444	9	US-09-893-519A-112	Sequence 112, App
10	59.4		657	10	US-09-974-300-1107	Sequence 1107, Ap
11	56.4		3606	7	US-08-781-986A-43	Sequence 43, Appl
12	56		2508	10	US-09-934-323-3	Sequence 3, Appli
13	56		4667	10	US-09-934-323-1	
14	55.4		2428	9	US-09-418-176-1	Sequence 1, Appli
15	55.4		2428	10	US-09-969-347-220	Sequence 220, App
16	55.2		2191	9	US-09-954-531-1038	38
17	55.2	3.2	2191	10	US-09-880-107-3854	
18	55.2	3. 2	2484	9	US-10-102-806-271	Sequence 271, App
19	53.8	3.1	1470	10	US-09-894-991-1	Sequence 1, Appli

1 1470 10 US-09-894-991 1 1641 10 US-09-895-860 1 2087 10 US-09-895-860 1 3824 9 US-10-026-072- 1 3824 9 US-10-123-904- 1 3824 9 US-10-123-904- 1 3824 9 US-10-175-746- 1 3824 9 US-10-175-746- 1 3824 9 US-10-176-918- 1 3824 9 US-10-176-918- 1 3824 9 US-10-176-918- 1 3824 9 US-10-176-921- 1 3824 9 US-10-137-865- 1 3824 9 US-10-142-431- 1 3824 9 US-10-142-419- 1 3824 9 US-10-142-419- 1 3824 9 US-10-142-419-	8 3.1 1470 10 US-09-894-991-7  8 3.1 1641 10 US-09-895-860-3  8 3.1 2087 10 US-09-895-860-3  8 3.1 3824 9 US-10-028-072-541 S  8 3.1 3824 9 US-10-028-072-541 S  8 3.1 3824 9 US-10-123-904-541 S  8 3.1 3824 9 US-10-123-904-541 S  8 3.1 3824 9 US-10-176-918-541 S  8 3.1 3824 9 US-10-137-865-541 S  8 3.1 3824 9 US-10-142-431-541 S	7	ഗ	ر ت	ر ت	5	5	ر ت	5	ر ت	5	ر ت	s	33 5	ر د	ر. ت	Ct.	5	5	ر ت	ر ت	5	5	5	5	ر ت	J
1470 10 US-09-894-99 1641 10 US-09-895-81 2087 10 US-09-895-81 3824 9 US-10-028-04 3824 9 US-10-028-05 3824 9 US-10-121-04 3824 9 US-10-121-04 3824 9 US-10-176-91 3824 9 US-10-176-92 3824 9 US-10-176-92 3824 9 US-10-176-92 3824 9 US-10-176-92 3824 9 US-10-127-88 3824 9 US-10-127-89 3824 9 US-10-127-89 3824 9 US-10-137-86 3824 9 US-10-137-86 3824 9 US-10-140-47 3824 9 US-10-142-43 3824 9 US-10-142-43 3824 9 US-10-143-11 3824 9 US-10-143-11 3824 9 US-10-143-11 3824 9 US-10-143-11 3824 9 US-10-143-16 3824 9 US-10-143-16 3824 9 US-10-140-00 3824 9 US-10-140-00 3824 9 US-10-140-00 3824 9 US-10-140-00 3824 9 US-10-140-16 3824 9 US-10-140-16 3824 9 US-10-140-16	1 1470 10 US-09-894-991-7 1 1641 10 US-09-895-860-3 1 2087 10 US-09-895-860-3 1 2087 10 US-09-895-860-3 1 3824 9 US-10-028-072-541 1 3824 9 US-10-035-855-22 1 3824 9 US-10-121-049-541 1 3824 9 US-10-121-049-541 1 3824 9 US-10-176-746-541 1 3824 9 US-10-176-746-541 1 3824 9 US-10-176-918-541 1 3824 9 US-10-176-918-541 1 3824 9 US-10-176-918-541 1 3824 9 US-10-176-918-541 1 3824 9 US-10-127-884-209 1 3824 9 US-10-127-865-541 1 3824 9 US-10-127-865-541 1 3824 9 US-10-137-865-541 1 3824 9 US-10-140-474-541 1 3824 9 US-10-140-474-541 1 3824 9 US-10-142-419-541 1 3824 9 US-10-140-160-22 1 3824 9 US-10-140-160-22 1 3824 9 US-10-140-160-22 1 3824 9 US-10-1230-163-209 1 3824 9 US-10-1230-163-209 1 3824 9 US-10-128-631-209 1 3824 9 US-10-230-163-309 1 3824 9 US-10-230-38-209														٠					•	٠			•		٠	•
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US-09-894-99 US-09-895-88 US-10-036-0A1 US-11-028-07 US-11-028-07 US-11-121-0A2 US-11-121-0A35-85 US-11-140-477 US-09-931-83 US-11-176-931	US-09-894-991-7 US-09-895-860-1 US-09-895-860-1 US-10-036-041-22 US-110-036-072-541 US-110-038-072-541 US-110-123-904-541 US-110-113-904-541 US-10-1175-746-541 US-10-175-746-541 US-10-176-918-541 US-10-176-921-541 US-10-176-931-931 US-10-176-931 US																										
-09-894-99 -09-895-88 -09-895-88 -09-895-88 -01-028-04	-09-894-991-7 -09-895-860-3 -09-895-860-3 10-036-041-22 10-036-041-22 10-121-049-541	SŪ	Sū	SD	SD	S	SD	SD	S	Sn	Sn	Sn	S	S	SU	S	S	Sn	US-	US	SU	US	SD	us-	S		
	Sequence Sequence	10-230-33	-218-63	142-41	10-036-16	140-00	-230-16	143-11	10-142-431-5	-035-719-2	10-140-474-5	10-137-865-5	10-036-214-2	10-227-884-	10-176-921-	10-176-918-	10-175-746-	931-836-	-140-470	-123-904	-121-049	035-855	028-072-	036-041-2	-09-895-860-	-09-895-860-	-09-894-991

## ALIGNMENTS

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RESULT 1

US-10-083-590-13

Sequence 13, Application US/10083590

Publication No. US20030027257A1

GENERAL INFORMATION:
APPLICANT: IATROU, Kostas
APPLICANT: IATROU, Kostas
APPLICANT: BEHIE, Leo A.

TITLE OF INVENTION: SEQUENCES FOR IMPROVING THE EFFICIENCY OF SECRETION OF TITLE OF INVENTION: NON-SECRETED PROTEINS FROM MAMMALIAN AND INSECT CELLS
FILE REFERENCE: 028722-207

CURRENT APPLICATION NUMBER: US/10/083,590

CURRENT FILING DATE: 2002-02-27

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/256,694

PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-24

PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-20

PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-20

PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-21

NUMBER OF SEQ ID NOS: 14

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LENGTH: 1691
TYPE: DNA
ORGANISM: Heliothis virescens
                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
                                                                                                                                                                                                             380
                                                                                                                                                                                                                                   368 CCGAAACTAAACGTCCCGTTTTAGTATACATACATGGTGGTGGTGTTTTATTATTATCGGTGAAA 427
                                                                                                      440 GCCACGAGGACCTACACGGACCAGAATATTTGGTCACTAAGAATGTCATCGTCATCACGT 499
                                                                                                                                 428 ATCATCGTGATATGTATGGTCCTGATTATTTCATTAAAAAAGGATGTGGTGTTGATTAACA 487
500 TTAATTACAGATTGAACGTCTTCGGTTTCCTGTCCATGAACACAACA-----AAAATCC 553
                                                                                                                                                                                                                                                                                                            Local Similarity
mes 210; Conserv
                                                  TACAATATCGTTTGGGAGCTCTAGGTTTTCTAAGTTTAAATTCAGAAGACCTTAATGTGC 547
                                                                                                                                                                                                        CCACACCTTTACGGCCTATCCTGGTGTTCATACATGGTGGAGGATTTGCTTTCGGCTCCG 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Ver.
                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                  5.1%; Score 87.2; DB 9; 53.3%; Pred. No. 1.9e-12;
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                                                                                                                                                                                                                                                                                                            Mismatches 178;
                                                                                                                                                                                                                                                                                                                                                            Length 1691;
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RESULT 2 US-09-738-626-1254

GENERAL INFORMATION:

APPLICANT: NAKAGAWA, SATOSHI APPLICANT: MIZOGUCHI, HIROS

MIZOGUCHI, HIROSHI ANDO, SEIKO

APPLICANT:
APPLICANT:

APPLICANT:

APPLICANT:
APPLICANT:

APPLICANT:

OZAKI, AKIO TATEISHI, NAOKO SENOH, AKIHIRO YOKOI, HARUHIKO HAYASHI, MIKIRO

IKEDA, MASATO

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PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Corynebacterium glutamicum us-09-738-626-1254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1254, Application US/09738626 Publication No. US20020197605A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     734 TGAGCGGAACAGGAATGAGCTACTTCTTTACTAC 767
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTACCCACTACATGATGTTAACCGAACAAACTCGCGGTCTTTTCCATCGTGGTATACTAA
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                                                                                                                                                                                                                                                                                              GGGTATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCACCCCCAGCGACC 236
                                                                                                                                            TGATTTTATAACGGGCAAAGTGTGTGTGGGCTCAGAGGGATTGTCTATACCTAAGTGTCTATAC
                                                                                                                                                                                          CAAGAAATGGGACGGCGTGCGCGATTGCTCAATGTTCGGTGAAGTAGCTTCTCAGCCAAC
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                                                                                                                                                                                                                                                              GGGAATTCCCTACGGCCGAAACACTGGCGGAAAATATCGCTTCCGGGCACCCCGGCCCGC 137
TATTATCGGTGA----AAATCATCGTGATATGTATGGTCCTGATTATTTCATTAAAAAAGGA 470
                                                   G-----CCTGATTCCGAAGAAAAGCTTCCTGTTGTGGTGTATCTCCACGGCGGTTCCTT
                                                                                    GTACTCCTGGACAGATAAGATTCGCGGTTCAGAAGACTGCCTTAACCTCGATGTCGTGCG
                                                                                                                                                                                                                                                                                                                                                       Score 78.8; DB 9;
pred. No. 2.7e-10;
                                                                                                                                                                                                                                                                                                                                        Mismatches 262;
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; NAME/KEY: CDS
; LOCATION: (86)...(1891)
US-09-748-739A-1
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SEQ ID NO 1
LENGTH: 1967
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APPLICANT: Watkins, Jeffry D.
APPLICANT: Watkins, Jeffry D.
APPLICANT: Watkins, Jeffry D.
APPLICANT: Watkins, Jeffry D.
APPLICANT: Watkins Jeffry D.
APPLICANTION: Methods of Use
TITLE OF INVENTION: Methods of Use
TITLE REFERENCE: P-TX 4143
CURRENT APPLICATION NUMBER: US/09/748,739A
CURRENT APPLICATION NUMBER: 2000-12-06
NUMBER OF SEQ. ID NOS: 31
NUMBER OF SEQ. ID NOS: 31
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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OTHER INFORMATION: Human Butyrylcholinesterase variant
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                                                                                                                                                                                                                                                                                        GTTTTAGTATACATACATGGTGGTGGTTTTATTATCGGTGAAAATCATCGTGATATGTAT 444
                                                                                                                                                                                                                                                                    GTATTGATATGGATTTATGGTGGTGGTTTTCAAACTGGAACATCATCTTTACATGTTTAT 553
                                                                                                                                                              GGAGCTCTAGGTTTTCTAAGTTTAAATTCAGAAGACCTTAATGTGCCCGGTAATGCCGGC 561
                         AATCCCGATAATATTACAGTCTTTGGTGAAAGTGCCGGTGCTGCCTC
                                                           TTATTTGATCAACAGTTGGCTCTTCAGTGGGTTCAAAAAAATATAGCAGCCTTTGGTGGA
                                                                                            CTTAAAGATCAAGTCATGGCCTTGCATTGGATTAAAAATAATTGCGCCCAACTTTGGTGGC
                                                                                                                               GGTGCCCTAGGATTCTTAGCTTT----GCCAGGAAATCCTGAGGCTCCAGGGAACATGGGT 670
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Pred. No. 2.3e-06;
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SOFTWARE: PatentIn ver-SEQ ID NO 1254 LENGTH: 1611

TYPE: DNA

Best Loc Matches

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Query Match

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                                                                                                                                    Sequence 3, Application US/09748739A Patent No. US20020119489A1 GENERAL INFORMATION:
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SEQ ID NO 2271
LENGTH: 2381
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2271, Application Patent No. US20020142981A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 191;
APPLICANT: Lockridge, Oksana
APPLICANT: Watkins, Jeffry D.
TITLE OF INVENTION: Butyricholinesterase Variants
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: P-IX 4113
CURRENT APPLICATION NUMBER: US/09/748,739A
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Horne, Darci T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Genbank Accession No. US20020142981A1 M16474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                         502 GGAGCTCTAGGTTTTCTAAGTTTAAATTCAGAAGACCTTAATGTGCCCGGTAATGCCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                        544 GATGGCAAGTTTCTGGCTCGGGTTGAAAGAGTTATTGTAGTGTCAATGAACTATAGGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        427 GAAGACTGTTTATATCTAAATGTATGGATTCCAGCACCTAAACC---AAAAAATGCCACT 483
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                                                                                                                                                                                                                                                                                                                        TTATTTGATCAACAGTTGGCTCTTCAGTGGGTTCAAAAAAATATAGCAGCCTTTGGTGGA
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Pred. No. 2.6e-06;
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TYPE: DNA
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; NAME/KEY: CDS
; LOCATION: (214)...(1935)
US-09-748-739A-3
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LENGTH: 2416
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Best Local Similarity 55.0%;
Matches 191; Conservative
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                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/09748739A Patent No. US20020119489A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: P-IX 4143
CURRENT APPLICATION NUMBER: US/09/748,739A
CURRENT FILING DATE: 2000-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lockridge, Oksana
APPLICANT: Watkins, Jeffry D.
TITLE OF INVENTION: Butyrylcholinesterase Variants
TITLE OF INVENTION: Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: (214)...(1935)
                                                                                                                                                                                                                                                                            OTHER INFORMATION: Human
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                          325 GAGGATTGTCTATACCTAAGTGTCTATACGAATAATCTAAATCCCGAAACTAAACGTCCC 384
481 GAAGACTGTTTATATCTAAATGTATGGATTCCAGCACCTAAACC---AAAAAATGCCACT 537
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                                                                                            Conservative
                                                                                                               3.7%;
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Pred. No. 2.6e-06;
                                                                                                               Score 63.8; DB 10;
Pred. No. 2.6e-06;
                                                                                            Mismatches
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RESULT 7 US-09-748-739A-7

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; NAME/KEY: CDS
; LOCATION: (214)...(1935)
US-09-748-739A-7
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APPLICANT: Lockridge, Oksana
APPLICANT: Watkins, Jeffry D.
APPLICANT: Watkins, Jeffry D.
TITLE OF INVENTION: Butyrylcholinesterase Variants
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: P-IX 4143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/09748739A Patent No. US20020119489A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 2416
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CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE: OTHER INFORMATION: Human Butyrylcholinesterase variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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                                                                                                                                                GGAGCTCTAGGTTTTCTAAGTTTAAATTCAGAAGACCTTAATGTGCCCGGTAATGCCGGC
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ANTCCCGATAATATTACAGTCTTTGGTGAAAGTGCCGGTGCTTC
                                                                                    CTTAAAGATCAAGTCATGGCCTTGCATTGGATTAAAAATAATTGCGCCCAACTTTGGTGGC
                                                                                                                           GGTGCCCTAGGATTCTTAGCTTT----GCCAGGAAATCCTGAGGCTCCAGGGAACATGGGT
                                                       TTATTTGATCAACAGTTGGCTCTTCAGTGGGTTCAAAAAAATATAGCAGCCTTTGGTGGA
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nilarity 55.0%;
Conservative
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Pred. No. 2.6e-06;
0; Mismatches 147;
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US-09-748-739A-16
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LENGTH: 2416
TYPE: DIA
ORGANISM: Homo sapiens
US-09-748-739A-16
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; Sequence 112, Application US/09893519A
; Publication No. US20030027243A1
; GENERAL INFORMATION:
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APPLICANT: Watkins, Jeffry D.
TITLE OF INVENTION: Butyrylcholinesterase Variants and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: P-IX 4143
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Best Local Similarity 55.0%;
Matches 191; Conservative
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CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT:
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DESILVA, Thamara
HARRIS, Sandra
KOMARNITSKY, Svetlana
MENDILLO, Marc
                                                                                                                                                                                                                                                                                                        ANADYS PHARMACEUTICALS,
                                                                                                                                                                                                                                                                        THOMPSON, Craig
MOORE, Jeffrey
                                                                                      HAQ,
                                                                     ZHU,
                                                                                                                                                                                                                                                  BUURMAN, Ed T.
                                                                                                        SANDERSON, Karen
                                                                                                                           MCCOY, Melissa
                                DAVIDOV, Eugene
                                                                     Shuhao
                                                                                      Tariq
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Pred. No. 2.6e-06;
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Query Match Best Local Similarity Matches 191; Conserv

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TYPE: DNA

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                                                                                                                                                                                                                                                                                                                                                                    Sequence 1107, Application Patent No. US20020146721A1 GENERAL INFORMATION:
                                                                          NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1107
                                                                                                                                                                                                                    APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 191;
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Best Local
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ORGANISM: Bacillus licheniformis -09-974-300-1107
                                                                                                                                       PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
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ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/215,164 PRIOR FILING DATE: 2000-06-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.1
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DATABASE ENTRY DATE: 2001-02-03
RELEVANT RESIDUES: (1)..(2444)
                                                               LENGTH: 657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTCCTAAAAGTGTAACTCTCTTTGGAGAAAGTGCAGGAGCAGCATC
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Pred. No. 2
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2.6e-06;
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US-08-781-986A-43
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US-08-781-986A-43
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Query Match
Best Local Similarity
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                        TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION: NAME: Benson, Bob
                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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NUMBER OF SEQUENCES:
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                                                                               STRANDEDNESS:
                                                                                                                                                                                                         REGISTRATION NUMBER: 30, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                         FILING DATE
                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
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                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
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3.3%;
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Pred. No. 1
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56.4; DB 7;
No. 0.00027;
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GENERAL INFORMATION:

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RESULT 13
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Sequence 1, Application US Patent No. US20020150910A1
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LENGTH: 2508
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Best Local Similarity
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TITLE OF INVENTION: 33410, A NOVEL HUMAN CARBOXYLESTERASE
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
FILE REFERENCE: 10448-081001
CURRENT APPLICATION NUMBER: US/09/934,323
CURRENT FILING DATE: 2001-08-21
CURRENT FILING DATE: 2001-08-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/226,774
PRIOR FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                  TCCATCGTGGTATACTAATGTCGGGTAATGCTATTT 745
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                   US/09934323
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; LOCATION: (420)...(2924)
US-09-934-323-1
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PRIOR FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09418176 Publication No. US20030040040A1
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Best Local Similarity
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TITLE OF INVENTION: 33410, A MOVEL HUMAN CARBOXYLESTERASE
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
FILE REFERENCE: 10448-081001
CURRENT APPLICATION NUMBER: US/09/934,323
CURRENT FILING DATE: 2001-08-21
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TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1210
                                                             FILING DATE: 04-APR-1996 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Das, Goutam
TITLE OF INVENTION: DNA Molecule
TITLE OF INVENTION: Polypeptides
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                                                                                                                            PRIOR APPLICATION DATA:
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ADDRESSEE: White & Case
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APPLICATION NUMBER: PCT/
FILING DATE: 12-MAR-1996
NIOR APPLICATION DATA:
                                                                                                                                                     CLASSIFICATION:
                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                CITY: New York
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10036-2787
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53.7%;
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                                             PCT/SE96/00318
                                                                                                          08/624,398
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TELEFAX: (212) 354-811
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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NAME/KEY:
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NAME/KEY:
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NAME/KEY:
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ORIGINAL SOURCE:
ORGANISM: Homo sapiens
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NAME/KEY:
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ATTORNEY/AGENT INFORMATION:
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LOCATION:
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LOCATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: double
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REFERENCE/DOCKET NUMBER: 11
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1576..2415
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1174..1377
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1921..1953
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1888..1920
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1822..1854
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US-09-969-347-220
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Patent NV. VILLEY GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ebner, Reinhard
APPLICANT: Ebner, Reinhard
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-69
FULT REPERENCE: 689290-69
CURRENT APPLICATION NUMBER: US/09/969,347
                                                                                                                            Sequence 220, Application US/09969347 Patent No. US20020115085A1
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Best Local :
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PUBLICATION INFORMATION:
AUTHORS: Nilsson
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PRIOR APPLICATION NUMBER: US/60/237,598
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US/60/237,604
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 318
SOFTWARE: Patentin version 3.0
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LENGTH: 2428
TYPE: DNA
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## SUMMARIES

AR06-2837 AR15-3441 LCU5-6636 AR15-3442 AR15-3438 AR15-3439 AR15-3439	R06283 R15344 S6636 R15344 R15343 R15343
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## ALIGNMENTS

TITLE	REFERENCE AUTHORS		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AR062837	RESULT 1
Boyce, T. Mark., Campbell, P. Malcolm., Parker, A. Gerard., Oakeshott, J. Graham. and Smyth, KA. Enzyme based bioremediation	<pre>1 (bases 1 to 1713) Russell,R.Joyce., Newcomb,R.David., Robin,G.Charlesde.Quetteville.,</pre>	Unclassified.	Inknown	Unknown.	•	AR062837.1 GI:5990528	AR062837	Sequence 1 from patent US 5843758.	AR062837 1713 bp DNA		
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Russell,R.Joyce., Newcomb,R.David., Campbell,P.MalcolRobin,G.Charlesde.Quetteville., Claudianos,C., Smyth, Boyce,T.Mark., Oakeshott,J.Graham. and Brownlie,J.ColMalathion carboxylesterase
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Eukaryota; Bndopterygota; Diptera; Brachycera;
Neoptera; Endopterygota; Lucilia.
Oestroidea; Calliphoridae; Lucilia.
1 (bases 1 to 2240) 96392952 U56636.1 LCU56636 (bases cuprina GI:1336079 6 2240 bp alpha esterase ( resistant resistance, complete cds. (LcaE7) mRNA, Insecta; linear inear INV implicated Muscomorpha; with 10-JAN-2002 in

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Two different amino acid substitutions in the all-esterase, E3,
confer alternative types of organophosphorus insecticide resistance
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Mol. Biol. 27 (1), 15-25 (1997) 97215578
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345. .537
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/KIRNSlation="MNENVSLMEKLKWKIKCIENKFLNYRLTINETVVAETEYGKVKG
VKRLTYVDDSYYSFEGIPYAQPPVGELRFKAPORPTPWDGVROCCNHKDKSVQVDFIT
GKVCGSEDCLYLSVYINNLNPETKRPVLVYIHGGGFIIGENHRDMYGPDYFIKKDVVL
INIQYRLGALGFLSLMSEDLNVPGNAGLKDQVMALKWIKNNCANFGGUPDNITVFGS
GAAASTHYMMLTEQTRGLEHRGILMSGNAICPMANTQCHRAFTLAKLAGYKGEDNDK
SQLEFLMKARKPQDLIKLEEKVLTLEERTNKVMFPFGFTVEPYCTADCVLPKHFREMVK
DVLEFLMKARKPQDLIKLEEKVLTLEERTNKVMFPFGFTVEPYCTADCVLPKHFREMVK
TAMGNSIPTMMGNTSYEGLFFTSILKQMPMLVKELETCVNFVPSELADAERTAPETLE
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658. .808
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EDLINPYRIMRSGRGVKGVSHADELTYEFWNQLAKRMPKESREYKTIERMTGIWIQFA
TTGNPYSNEIEGMENVSWDPIKKSDEVYKCLNISDELKMIDVPEMDKIKQWESMFEKH
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298. .2010
                                                        /note-"organophosphorus insecticide resistance malathion" % \left( \frac{1}{2}\right) =\frac{1}{2}\left( \frac{1}{2}\right) \left( \frac{1}{2}\right) 
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	exon 1540>2010 /gene="LCaE7"
BASE ORIGI	357 c
Que Bes Mat	ry Match 100.0%; Score 1713; DB 3; Length 2240; It Local Similarity 100.0%; Pred. No. 0; Caps 1713; Conservative 0; Mismatches 0; Indels 0; Gaps
Qу	1 ATGAATTTCAACGTTAGTTTGATGGAGAAATTAAAATGGAAGATTAAAATGCATTGAAAAT 60 
Оу	61 AAGTTTTTAAACTATCGTTTAACTACCAATGAAACGGTGGTAGCTGAAACTGAATATGGC 120
P 89	121 AAAGTGAAAGGCGTTAAACGTTTAACTGTGTACGATGATTCCTACTACAGTTTTGAGGGT 180
Dy Oy	B1 ATACCGTACGCCCAACCGCCAGTGGGTGAGGTGAGATTTAA
Qy	41 CCCTGGGATGGTGTGGTGATTGTTGCATAAAGATAAGTCAGTGCAI
рь	AAAGATAAGTCAGTGCAAGTTGAJ
P 69	301 ATAACGGGCAAAGTGTGTGGGTCAGAGGATTGTCTATACCTAAGTGTCTATACGAATAAT 360 301 ATAACGGGCAAAGTGTGTGGGCTCAGAGGATTTGTCTATACCTAAGTGTTGTTATACGAATAAT 657 598 ATAACGGGCAAGTGTTGTGCTCTCAGAGGATTGTCTATACCTAAGTGTTCTATACGAATAAT 657
Qy	9
0 !	21 CCTCAAAAATCATCCTCATATCTATCCTCCTGATTATTTCATTAAAAAAGGATGTGGTGTTG 4
Вb	
Qy	81 ATTAACATAC
DЬ	TTAACATACAATATCGTTTGGGAGCTCTTAGGTTTTCTAAGTTTAAATTCAGAAGACCT
Qy	4
Db	38 AATGTGCCCGGTAATGCCGGCCTTAAAGATCAAGTCATGCTTGTGTGTG
DB Qy	601 ANTIGGCCAACTITGGTGGCAATCCCGATAATATATACAGTCTTTGGTGAAAGTGCCGGT 640   11111111111111111111111111111111111
Qy	661 GCTGCCTCTACCCACTACATGATGTTAACCGAACAAACTCGCGGGTCTTTTCCATCGTGGT 720
DЬ	58 GUTGCCTCTACCCACTACATGATGTTAACCGAACAAACTCGCGGTCTTTTCCATCGTGGT 10
Qy	21 ATACTAATGTCGGGTAATGCTATTTGTCCATGGGCTAATACCCCAATGTCAACATCGTGCC 78
Db	TACTAATGTCGGGTAATGCTATTTGTCCATGGGCTAATACCCAATGTCAACATCGTGCC 1
Qy	781 TTCACCTTAGCCAAATTGGCCGGCTATAAGGGTGAGGATAATGATAAGGATGTTTTGGAA 840
Дb	TCACCTTAGCCAAATTGGCCGGCTATAAGGGTGAGGATAATGATAAGGATGTTTTGGAA II
ph yo	841 TTTCTTATGAAAGCCAAGCCACAGGATTTAATAAAACTTGAGGAAAAAGTTTTAACTCTA 900
Qy	901 GAAGAGCGTACAAATAAGGTCATGTTTCCTTTTTGGTCCCACTGTTGAGCCCATATCAGACC 960

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RESULT 4
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DEFINITION
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VERSION
KEYWORDS
SOURCE
         TITLE
JOURNAL
FEATURES
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                                                             AUTHORS
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        1 (bases 1 to 1713)
1 (bases 1 to 1713)
Russell,R.Joyce., Newcomb,R.David., Campbell,P.Malcolm.Robin,G.Charlesde.Quetteville., Claudianos,C., Smyth,K.Boyce,T.Mark., Oakeshott,J.Graham. and Brownlie,J.Colin Malathion carboxylesterase
Patent: US 6235515-A 9 22-MAY-2001;
Location/Qualifiers
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Russell R.Joyce., Newcomb, R.David., Campbell, P.Malcolm., Russell R.Joyce., Newcomb, Claudianos, C., Smyth, K.-A., Robin, G. Charlesde, Quetteville., Claudianos, C., Smyth, K.-A., Robin, G. Charlesde, Ouetteville., Claudianos, C., Smyth, K.-A., Robin, G. Charlesde, Ouetteville., Claudianos, C., Smyth, K.-A., Robin, G., Smyth, K.-A., Robin, Claudianos, C., Smyth, K.-A., Robin, C., Smyth, C., Sm
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Sequence 1 from patent US 6235515.
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Location/Qualifiers 1.1713
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                          TTCACCTTAGCCAAATTGGCCGGCTATAAGGGTGAGGATAATGATAAGGATGTTTTGGAA
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Sequence 5 from patent US 6235515.
AR153440
AR153440.1 GI:15120972
                                                                                             1 (bases 1 to 1713)
1 (bases 1) to 1713)
Russell,R.Joyce.. Newcomb,R.David., Campbell,P.Malcolm.,
Russell,R.Joyce.. Revision, Claudianos,C., Smyth,K.-A.,
Robin,G.Charlesde.Quetteville., Claudianos,C., Smyth,K.-A.,
Boyce,T.Mark., Obkeshott,J.Graham. and Brownlie,J.Colin.
Malathion carboxylesterase
Malathion carboxylesterase
Malathion carboxylesterase
Location/Qualifiers
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1 CAAATGCCTATGCTTAAGGAATTGGAAACTTGTCTCAATTTTCTGCCAAGTGAATTG	$\triangleright - \triangleright$	1 GCTGATTGTGTCTTACCCAAACATCCTCGGGAAATGGTTAAAACTGCTTGGGGTAATTCG 	1 GAAGAGCGTACAAATAAGGTCATGTTTCCTTTTGGTCCCACTGTTGAGCCATATCAGACC 	TTTCTTATGAAAGCCAAGCCACAGGATTTAATAAAACTTGAGGAAAAAGTTTTAACTCTA 	TTCACCTTAGCCAAATTGGCCGGCTATAAGGGTGAGGATAATGATAAGGATGTTTTGGAA 	ATACTAATGTCGGGTAATGCTATTTGTCCATGGGCTAATACCCAATGTCAACATCGTGCC 	GCTGCCTCTACCCACTACATGATGTTAACCGAACAAACTCGCGGTCTTTTCCATCGTGGT 	ARTTGCGCCAACTTTGGTGGCAATCCCGATAATATTACAGTCTTTGGTGAAAGTGCCGGT	. AATCTGCCCGGTAATGCCGGCCTTAAAGATCAAGTCATGGCCTTGCGTTGGATTAAAAAT 	ATTAACATACAATATCGTTTGGGAGCTCTAGGTTTTCTAAGTTTAAATTCAGAAGACCTT	GGTGAAAATCATCGTGATATGTATGGTCCTGATTATTTCATTAAAAAGGATGTGGTGTTG	CTAAATCCCGAAACTAAACGTCCCGTTTTAGTATACATAC	ATAACGGGCAAAGTGTGTGGCTCAGAGGATTGTCTATACCTAAGTGTCTATACGAATAAT	CCCTGGGATGGTGTGCGTGATTGTTGCAATCATAAAGATAAGTCAGTGCAAGTTGATTTT	ATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCACCCCAGCGACCAACA	AAAGTGAAAGGCGTTAAACGTTTAACTGTGTACGATGATTCCTACTACAGTTTTGAGGGT 	AAGTTTTTAAACTATCGTTTAACTACCAATGAAACGGTGGTAGCTGAAACTGAATATGGC	
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ATGAATTTCAACGTTAGTTTGATGGAGAAATTAAAATGGAAGATTAAATGCATTGÀAAAT 60 	Query Match 98.2%; Score 1683; DB 6; Length 1713; Best Local Similarity 98.2%; Pred. No. 0; Matches 1683; Conservative 0; Mismatches 30; Indels 0; Gaps 0;	source 1. 1713  /organism="unknown"  BASE COUNT 506 a 299 c 363 g 515 t 30 others  ORIGIN			AR062838.1 GI:5990529  Unknown. M Unknown.	AR062838 LOCUS AR062838 1713 bp DNA linear PAT 29-SEP-1999 DEFINITION Sequence 2 from patent US 5843758. ACCESSION AR062838		TCGATGTTTGAAAAACATAGAGATTTATTTAG 1713	1621 ATTAGTGACGAATTGAAAATGATTGATGTGCCTGAAATGGATAAGATTAAACAATGGGAA 1680 	1561 ATGGAAAATGTTTCCTGGGATCCAATTAAGAAATCCGACGAAGTATACAAGTGTTTGAAT 1620 		1441 AATCAATTGGCCAAACGTATGCCTAAAGAATCGCGTGAATACAAAACAATTGAACGTATG 1500 1501 ACTGGTATATGGATACAATTTGCCCACCACTGGTAATCCTTATAGCAATGAAATTGAAGGT 1560	1301 CGIAGIGGACGIGGIGITAAGGGIGITAGICAIGCIGAIGAAITAACCIAITTCITCIGG 1440 1441 AATCAATTGGCCAAACGTATGCCTAAAGAATCGCGTGAATACAAAACAATTGAACGTATG 1500 	CGTAGTGGACGTGGTGAAGGGTGTTAGTCATGCTGATGAATTAACCTATTTCTTCTGG 144	.321 GTCTACTTGTATCGCTTCGACTTTGATTCGGAAGATCTTATTAATCCCTATCGTATTATG 1380	261 TTCTGGTTCCCCATGCATCGTTTGTTGCAATTACGTTTCAATCACACCTCCGGTACACCC 1320	CATGTTACAGGAGAAACACCAACAGCTGATAATTTTATGGATCTTTGCTCTCACATCTAT	.141 GCTGATGCTGAACGCACCGCCCAGAGACCTTGGAAAATGGGTGCTAAAATTAAAAAGGCT 1200 .201 CATGTTACAGGAGAAACACCAACAGCTGATAATTTTATGGATCTTTTGCTCTCACATCTAT 1260	GCTGATGCTGAACGCACCGCCCCAGAGACCTTGGAAATGGGTGCTAAAATTAAAAAGGCT	TVOI CARAIGCCIAIGCIIGITAAGGAATTGGAAAACTTGTGACAATTTTGTGCCAAGTGAATTG 1140
Qy 1081 CAAATGCCTATGCTTAAGGAATTGGAAACTTGTGTCAATTTTTGTGCCAAGTGAATTG 1140	Qy 1021 ATACCCACTATGATGGGTAACACTTCATATGAGGGTCTATTTTTCACTTCAATTCTTAAG 1080	Qy 961 GCTGATTGTGTCTTACCCAAACATCCTCGGGAAATGGTTAAAACTGCTTGGGGTAATTCG 1020	QY 901 GAAGAGCGTACAAATAAGGTCATGTTTCCTTTTGGTCCCACTGTTGAGCCATATCAGACC 960	Qy 841 TTTCTTATGAAAGCCAAGGCACAGGATTTAATAAAACTTGAGGAAAAAGTTTTAACTCTA 900	Qy 781 TTCACCTTAGCCAAATTGGCCGGCTATAAGGGTGAGGATAATGATAAGGATGTTTTGGAA 840	Qy 721 ATACTAATGTCGGGTAATGCTATTTGTCCATGGGCTAATACCCAATGTCAACATCGTGCC 780.	Db 661 GCTGCCTCTACCCACTACATGATGTTAACCGAACAAACTGCGGGTCTTTTCCATCGTGGT 720		Db 541 AATGTGCCCNGTAATGCCGGCCTTAAAGATCAAGTCATGGCCTTGCGTTGGATTAAAAAT 600	Db 481 ATTAACATACAATATCGTTTGGGAGCTCTAGGTTTTCTAAGTTTAAATTCAGAAGACCTT 540  Qy 541 AATGTGCCCGGTAATGCCGGCCTTAAAGATCAAGTCATGGCCTTGCGTTGGATTAAAAAT 600	481 ATTAACATACAATATCGTTTGGGAGCTCTAGGTTTTCTAAGTTTAAATTCAGAAGACCTT	Qy 421 GGTGAAAATCATCGTGATATGTATGGTCCTGATTATTTCATTAAAAAGGATGTGGTGTG 480	QY 361 CTAAATCCCGAAACTAAACGTCCCGTTTTAGTATACATAC		Db 241 CCCTGGGATGGTGTGCATTGTTGCAATCATAAAGATAAGTCAGTGCAAGTTGATTTT 300  Qy 301 ATAACGGGCAAAGTGTGTGGCTCAGAGGATTGTCTATACCTAAGTGTCTATACGAATAAT 360	Db 181 ATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCACCCCAGCGACCNAACA 240  Qy 241 CCCTGGGATGGTGCGTGATTGTTGCCAATCATAAAGATAAGTCACTGCAAGTTGATTTT 300	– ×	Qy 121 AAAGTGAAAGGCGTTAAACGTTTAACTGTGTACGATGATTCCTACTACAGTTTTGAGGGT 180	2=	QY 61 AAGTTTTTAAACTATCGTTTAACTACCAATGAAACGGTGGTAGCTGAAACTGAATATGGC 120

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                                                                                                                                                                                                                                                                                                                          Claudianos, C., Russell, R.J. and Oakeshott, J.G. The same amino acid substitution in orthologous e organophosphate resistance on the house fly and a Insect Biochem. Mol. Biol. 29 (8), 675-686 (1999)
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                                                                                                                                                                                                                                    Claudianos, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Muscoidea; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Musca domestica
AF133341
AF133341.1 GI:
                                                                                                                                                                                            Direct Submission Submitted (07-MAR-1999)
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                                                                                                                                                                                                                                                           (bases 1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  domestica.
                                        /organism="Musca domestica"
/strain="Rutgers Diazinon-R
/db_xref="taxon:7370"
/chromosome="II"
/dev_stage="4 day third instar larvae"
1. .2160
                                                                                                                                               Location/Qualifiers
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Local Similarity
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                                                                            AATGTGCCCGGTAATGCCGGCCTTAAAAGATCAAGTCATGGCCTTGCGTTGGATTAAAAAT
                                                                                                                        GTAACCGTGCAATATCGTTTGGGTGTGTTGGGTTTCCTTAGCCTGAAATCGGAAAATCTC
                                                                                                                                        ATTAACAATACAATATCGTTTGGGAGCTCTAGGTTTTCTAAGTTTAAATTCAGAAGACCTT
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AATATTACCAATTTCGGTGGCGATGTAGACAATATTACCGTCTTCGGCGAAAGTGCTGGT
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/gene="MdaE7"
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GNSGSEDCLYLNYYNNLNIDTKRPULVFFIGGFICFGANRNYYGADDYFIKDVUF
GNSGSEDCLYLNYTNNLNIDTKRPULVFFIGFFIKNOCASFGCDDDCTFLFGES
TYQYRLGVLGFLSLMSENLAVPGNAGLKDQVMALRWIKNCASFGCDDDCTFLFGES
AGAASTHYMMITEQARGLFHRAVLMSGTAMCIWAHTQCQHRGYTIAKRIGYKGENNDK
DVYDFLMKANPYDLAREEHKVLTNEELRDKVWFAFGFTTEPYETPDCYLPKPMREMLK
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EEIINPYRIMRYGROVKGASHTDELTYLFWYMLSKKWPKDSRBYKTIERMIGIWTOFA.
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/protein_id="AAF14517.1"
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Russell,R.Joyce, Newcomb,R.David., Campbell,P.Malcolm.,
Russell,R.Joyce, Newcomb,R.David., Claudianos,C., Smyth,K.-A.,
Robin,G.Charlesde.Quetteville., Claudianos,C., Smyth,K.-A.,
Boyce,T.Mark., Oakeshott,J.Graham. and Brownlie,J.Colin.
Boyce,T.Mark., Oakeshott,J.Graham. and Brownlie,J.Colin.
Malathion carboxylesterase
Malathion carboxylesterase
Patent: US 6235515-A 14 22 MAY-2001;
Location/Qualifiers
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KEYWORDS
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    source
                                                         This clone was sequenced as part of a high-throughput process to sequence clones from Drosophila Gene Collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyh tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular cDNA clone. However, there are artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAs, and reverse transcriptase errors that result in single base changes. For further information about this sequence, including its location and relationship to other sequences, please visit our Web site (http://fruitfly.berkeley.edu) or send email to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCAATGAAATTGAAGGTATGGAAAATGTTTCCTGGGATCCAATTAAGAAATCCGACGAAG
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Lawrence Berkeley National
Berkeley, CA 94720
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 2017)

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                                              cdna@fruitfly.berkeley.edu.
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//db_xref="MIXBLASE:FB9n0015575"
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VTIQYRLGALGFWSLKSPELINVFENALGENGLKDQVLALKWIKNUCASFGODPNCITYFGES
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Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley, CA 94720
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Location/Qualifiers
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VVISYRLGALGFLSLADEELDVPGNAGLKDQVMALRWVKRNCQFFGGDPDNITVFGES
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DSKHFNIMRIITCGRKVRGTCHADDLSYLFYNAAAKKLKRRTAEFKTIKRLVSMVVHF
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/protein_id="AAM52002.1"
/db_xref="GI:21464398"
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/codon_start=1
                                                                                                                                AISGDPNIPMVCQDEKEQPRGAWLPISKDDKVFQCLNISHDVHVIDLPEAEKLRLWDC
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/db_xref="FLYBASE:FBgn0015576"
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/strain="y; cn bw sp"
/db_xref="taxon:7227"
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                                                                                                                                                                            ACCATGTTCAGCTTTGGACCCACCATCGAGCCCTATTTGACTCCTCATTGTGTGATTCCC
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                                                                                                                                                                                                                                                                                                               GGCTACACAGAGATGCTAACGATCGGGACATTTTTGCCCATCTCAAGAAATGTAGGGCC
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                                                                   AACACTTCATATGAGGGTCTATTTTTCACTTCAATTCTTAAGCAAATGCCTATGCTTGTT 1098
                                                                                                     AAGTCGCCACTGGAAATGATGCGGGACTGTTGGGGGCAACAGCATTCCCATGGTCATCGGA
                                                                                                                                        AAACATCCTCGGGAAATGGTTAAAACTGCTTGGGGTAATTCGATACCCACTATGATGGGT 1038
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Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
Neoptera; Endopterygota; Diptera; Drosophila.
Ephydroidea; Drosophiladae; Drosophila.
                                                                                   Submitted (11-MAR-1996) Charles
Entomology, Clunies Ross Street,
Location/Qualifiers
                                                                                                                                                                       Robin,C., Medveczky,K.M., Russell,R.J. and Duplication and Divergence of the genes of cluster of Drosophila melanogaster J. Mol. Evol. (1996) In press
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                                                                                  GTGCAAGTTGATTTTATAACGGGCAAAGTGTGTGGCTCAGAGGATTGTCTATACCTAAGT
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 57335)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence was identified as CDM:10213452 by
For further information on this sequence e-mail
* NOTE: This is a 'working draft' sequence
* This sequence will be replaced
* by the finished sequence as soon as it is avai
* the accession number will be preserved.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (16-NOV-1999) Celera Genomics, Rockville, MD, USA
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Drosophila melanogaster.
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AC015272
AC015272.1 GI:6436063
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/db_xref="taxon:7227"
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Pred. No. 1.8e-72;
0; Mismatches 614;
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to fly@celera.
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1217	TGGAAATGGGTGCTAAAATTAAAAAGGCTCATGTTACAGGAGAAAC	1158	Qγ
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35282	CACTTCGTACGAGGCCTGCTGTGGGTTCCAGGTTAGATATTGGGAATTTTTTTGAATT	<b>ω</b>	8
1058	ACACTTCATATGAGGGTCT	104	Qy
35342	CCGCCTGGAGTAACTCCATCCCCATGTTTATAGGAA	35401	В
1039	ACATCCTCGGGAAATGGTTAAAACTGCTTGGGGTAATTCGATACCCCACTATGATGGGTA	980	Qy
US .	CCATTCTCCACGCCCGAATGTGTGATATCCA	35461	рb
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Search completed: April 11, 2003, 06:05:47 Job time: 3038.03 secs

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Result
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## ALIGNMENTS

RESULT 1 AAQ91561 Boyce TM, Parker AG, Key WO9519440-A1 SS. 13-JAN-1994; 13-JAN-1995; 20-JUL-1995. Lucilia cuprina Esterase; E3; bioremediation; organophosphate; carbamate; insecticide; pesticide; water decontamination; meat decon OP-sensitive esterase E3 Lc743 clone 22-DEC-1995 AAQ91561; AAQ91561 standard; cDNA; 1713 BP (CSIR ) COMMONWEALTH SCI & IND RES ORG Campbell PM, Newcomb RD, Oakeshott JG; Robin GC, Russell RJ, Smyth K; (first entry) 94AU-0003347. 95WO-AU00016 Location/Qualifiers
1..1713 a meat decontamination;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA from organophosphate (OP)-sensitive L. cuprina pupa cDNA library was amplified using cluster-specific esterase primers. Isolated clone LC743, a probable full-length cDNA, was express using a baculovirus vector in insect cells and shown to encode an observation of a common content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of th
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phosphate and carbamate pes
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Pred. No. 0;
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RESULT 2
AAT68596
ID AAT6
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AC AAT6
XX
DT 08-P

standard;

DNA;

1713 BP

AAT68596;
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08-AUG-1997

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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                           DNA encoding enzyme that degrades organophosphate pesticides useful for decontamination of soil, water, food etc
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                                                             Sequence 1713 BP;
                                                                                                                     resistant enzyme acts as a malathion carboxylesterase and can be formulated for use in degrading environmental carboxylester or
                                                                                                                                                                                                                                                                                                                      Claim 4; Fig 1; 52pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Malathion carboxylesterase; organophosphate; insecticide; pesticide; remediation; bioremediation; decontamination;
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DB; AAW17765.
                                                                                                  general organophosphates
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D, Oakeshott JG,
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                                                         516 A; 305 C; 370 G; 522 T; 0 other;
  100.0%;
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(Trp
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JG, Robin GC,
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  Score 1713;
Pred. No. 0;
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Russell RJ,
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                                                                                                          AAQ91566
                                           CDS
                                                                       Esterase; E3; bioremediation; organophosphate; insecticide; pesticide; water decontamination;
                                                          Lucilia
         13-JAN-1995;
13-JAN-1994;
                             WO9519440-A1
                   20-JUL-1995
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Parker
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                                                                                                                                                                                                                                                                                                                                                                                                                          pure E3 esterase from Lucilia cuprina a
eliminate residues of organo:phosphate
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Similarity
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Robin GC, R
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                                                                                                                                                                                                                                                                                                                           Conservative
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Russell RJ,
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                                          RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding OP-susceptible esterase E3 of L. cuprina) from a diazinon resistant strain, Llandillo 103. 4 Isolated clones were sequenced (Lc7L103 A-D, AAQ91562-65) that encoded diazinin-resistant esterases. The esterases, or cells expressing them, are used in bioremediation.
                                                                                                                                                                                                       Example 4;
                                                                                                                                                                                                                                                                       Pure E3 esterase from eliminate residues of
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                                                                                                                                                                                                                                                      water,
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Robin GC, Russell RJ,
                                                                                                                                                                                                       Page 12-17;
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pesticide; water decontamination;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pure E3 esterase from Lucilia cuprina and related DNA - used to eliminate residues of organo:phosphate and carbamate pesticides
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                                              GCTGCCTCTACCCACTACATGTTAACCGAACAAACTCGCGGTCTTTTCCATCGTGGT
                AATTGCGCCAACTTTGGTGGCAATCCCGATAATATTACAGTCTTTGGTGAAAAGTGCCGGT
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98.7%;
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Pred. No. 0;
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                                                   CATGTTACAGGAGAAACACCAACAGCTGATAATTTTATGGATCTTTGCTCTCACATCTAT
                                                                                                                         GCTGATGCTGAACGCACCGCCCCAGAGACCTTGGAAATGGGTGCTAAAATTAAAAAGGCT
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A 1710 bp DNA molecule (AAT68597) comprises the Md-alpha-E7 coding sequence of the Musca domestica Rutgers strain. It was isolated by amplification of genomic DNA using alpha-esterase consensus primers (see also AAT68598-99) and use of a 534 bp amplicon to screen a genomic library of M. domestica. A mutation of the gene, resulting in substn. of serine for trypt at amino acid position 251 (see also AAW17767), confers malati
                                                                                                                                                                                                                               Key
mutation
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                                                                       encoding enzyme that degrades organophosphate pesticides ful for decontamination of soil, water, food etc
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DB; AAW17767.
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; remediation; bioremediation; decontamination;
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/*tag= a
/note= "Trp-251 TGG"
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73.4%;
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resistance. The resistant enzyme acts as a malathion carboxylesterase and can be formulated for use in degrading environmental carboxylester or dimethyl general organophosphates
449 T; 0 other;
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Score 956.6; DB 18; Pred. No. 5e-254; 0; Mismatches 444; Length 0; Gaps 0

AAAAGGATGTGGTGTGATTAACATACAATATCGTTTGGGAGCTCTAGGTTTTCTAAGTT GCGGAGATTTTATTTTCGGCGAAGCAAATCGTAACTGGTTTGGTCCCGACTACTTTATGA ATGTGTATACCAATGACTTGAACCCAGACAAAAGGCGTCCTGTTATGGTTTTCATCCATG 523 463 463 403

TGAAATCGGAAAATCTCAATGTCCCCGGCAACGCTGGCCTCAAGGATCAAGTAATGGCCT TAAATTCAGAAGACCTTAATGTGCCCGGTAATGCCGGCCTTAAAGATCAAGTCATGGCCT AGAAACCCGTGGTCTTGGTAACCGTGCAATATCGTTTGGGTGTTGGGTTTCCTTAGCC 643 583 583 523

TGAGATGGGTCAAGAGTAATATTGCCATTTTCGGTGGCGATGTAGACAATATTACCGTCT TGCGTTGGATTAAAAATAATTGCGCCAACTTTGGTGGCAATCCCGGATAATATTACAGTCT

TCGGCGAAAGTGCTGGTGGGGCCTCAACCCATTACATGATGATAACCGAACAGACCCGTG TTGGTGAAAGTGCCGGTGCTGCCTCTACCCACTACATGATGTTAACCGAACAAACTCGCG

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GTTTATTCCATCGTGGTATCATGATGTCCGGTAATTCCATGTGCTCATGGGCCTCTACAG GTCTTTTCCATCGTGGTATACTAATGTCGGGTAATGCCTATTTGTCCATGGGCTAATACCC

AATGTCAACATCGTGCCTTCACCTTAGCCAAATTGGCCGGCTATAAGGGTGAGGATAATG

823

763 763

AATGCCAAAGTCGTGCGCTCACCATGGCCAAACGTGTTGGCTATAAGGGAGAGGACAATG

ATAAGGATGTTTTGGAATTTCTTATGAAAGCCAAGCCACAGGATTTAATAAAACTTGAGG AAAAAGATATCCTGGAATTCCTAATGAAAGCCAATCCCTATGATTTGATCAAAGAGGAGC 883

TTGAGCCATATCAGACCGCTGATTGTGTCTTACCCAAACATCCTCGGGAAATGGTTAAAA CACAAGTTTTGACACCCGAAAGAATGCAAAATAAGGTCATGTTTCCTTTTGGACCCACTG AAAAAGTTTTAACTCTAGAAGAGCGTACAAATAAGGTCATGTTTCCTTTTGGTCCCACTG 943

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11-JUL-2000;
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2000US-0614150.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded proteins sequences (ABL018737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence data for this patent did not form part of the prispecification, but was obtained in electronic format directly at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 683; 21pp +
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                     AATGTGCCCGGTAATGCCGGCCTTAAAGATCAAGTCATGGCCTTGCGTTGGATTAAAAAT
                                                       GTCACGATACAGTACCGACTTGGGGCTTTGGGATTTATGAGTCTTAAGTCCCCCGAGCTA
                                                                   ATTAACATACAATATCGTTTGGGAGCTCTAGGTTTTCTAAGTTTAAATTCAGAAGACCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1704 BP;
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11-JUL-2000;
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                                                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaccutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG175) and the encoded proteins
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The sequence data for this patent did not form part of the specification, but was obtained in electronic format direct at ftp.wipo.int/pub/published\_pct\_sequences.

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                                     3954 TTGGCTACAAGGGCGAGGACAACGACAAGGATGTGCTGGAGTTCTTGCAGAACGTAAAGG
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                                                   CCGGCTATAAGGGTGAGGATAATGATAAGGATGTTTTGGAATTTCTTATGAAAGCCAAGC 859
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CACAGGATTTAATAAAACTTGAGGAAAAAGTTTTTAACTCTAGAAGAGCGTACAAATAAGG 919
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Db 4974 ATTTATTGT 4982
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nh 4914 TCGATCTGCCTGAGTGGCCCAAATTGAAGGTCTGGGAGAGCCTCTATGACGACAACAACC *2/2
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OY 1583 CAATTAAGAAATCCGACGAAGTATACAAGTGTTTGAATTATTAGAACTTGAAGTTCA 4913
Db 4794 CTGCCACGGGTAATCCCTACAGCGAGAAGATCAACGGGTAATTGAAAATGA 1642
QY 1523 CCACCACTGGTAATCCTTATAGCAATGAAAATTGAAGGTATGGACACTCTGACCCATTGATC 4853
Db 4734 CGAAGGAAAGTCGCGAGTACAGGAACATCGAACATCGAAAAATGTTTCCTGGGATC 1582
QY 1463 CTARAGARTCGCGTGARTACARARCARTTGARCGTATCTGGACCCAGTTTG 4793
Db 4674 GGGTCAGCCATGCCGACGATTTGAGCTACCAATTCACCATATAATGGATACAATTTG 1522
QY 1403 GTGTTAGTCATGCTGATGAATTAACCTATTTCTTCTCAAATCAACAGTCTGGCTCGCCGGTTGC 4733
Db 4614 TCGACTCCGAGGAGCTCATTTTTCCGTACCCCALIALSCCTATTCAATTCGCCAAACGTATGC 1462
Qy 1343 TTGATTCGGAAGATCTTATTAATCCCTATCGTATTATGCGAAGGACCCGGGTGTCAAGG 4673
Db 4554 TGGTCCATTCCCGACACGCGTACGCGCGCTACGCGCTCCTACGTCGTCGTGTTAAGG 1402
QY 1283 TGTTGCAATTACGTTTCAATCACACCTCCGGTACACCTACTATATATTTCTATCGATATATAT
Db 4494 AAGCTGGTAATTTATTTCAGCTCTGTTCGALLIAGLACTACTTGTATTCGCCTTCGACT 1342
QY 1243
Db 4434 AAGCACCCCAGATAATTACATGGATGTAAGTGTACGTTCCTCCATGCATCGTT 1282
QY 1218 ACCAACAGCTGATAATTTTATGGAT
QY 1158 CGCCCCAGAGACCTTGGAAATGGGTGCTAAAATTAAAAAGGCTCAGATTGGCTCAGA 4433
Db 4314 GCAGCAGCTTGATGCTGGCACACCTTTCATTCCAAAAAAAA
OY 1098 TAAGGAATTGGAAACTTGTGTCCAATTTTTGTGCCAAGTGAATTGGCCTAATTTGTGCCCAGTGAATTGGCCTAATTGGCCCAGGAGCCCAG 4373
Oy 1059
Db 4194 ACACTTCGTACGAGGGCCTGCTGTGGGTTCCAGGTTAGGGAAATGCCTATGCTTGT 1097
Qy 1040 ACACTTCATATGAGGGTCT
OY 980 AACATCCTCGGGAAATGGTTAAAAACTGCTTGGGGTAATTCGATACCTCATGTTTATAGGAA 4193
Db 4074 TAATGTTTGCCCTTGGCCCATCCCTGGAACCATICICCACCTCTATTGATGGGTA 1039
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                AGCACTTCGTGTTCGAGATGACCGATGGCTCCGAGGACTGCCTCTACCTCAATGTCTACA
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                                 CCTACTTGTTCTACAACTCGCTGGCGAGGAAGCTCAAGAACCACACGCGGGAGTACAAGT
                                                                   CCTATTTCTTCTGGAATCAATTGGCCAAACGTATGCCTAAAGAATCGCGTGAATACAAAA
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                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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P-PSDB; ABB60586.
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                                                                                                                                                                                                             The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                       Sequence 1792 BP;
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  The invention relates to an isolated nucleic capable of detecting 1000 or more genes from
                                                                            Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 791; 21pp + Sequence Listing; English
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genes from Drosophila and
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# ALIGNMENTS

FEATURES Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 778)
Harvey, D., Brokstedin, P., Hong, L., Evans-Holm, M., Su, C., Tsang, Lewis, S. and Rubin, G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
Contact: Stapleton, M. Lawrence Berkeley National Lab One Cyclotron Rd, Berkeley, CA 94720, USA Fax: 510 486 6798 Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu Plate: 10 row: G column: 4 High quality sequence stop: 36 . AIO62034 778 bp mRNA linear EST 19-APR-2001 GH01076.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH01076 5prime similar to US1050: Drosophila melanogaster alpha esterase (aE7) gene, partial cds,

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                                                                                                             GGCGCCTCCACTCACTACATGATGCTAA
A1388926 649 bp mRNA linear EST 19-APR-2001 GH19977.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH19977 5prime similar to U51050: Drosophila melanogaster alpha esterase (aE7) gene, partial cds,
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/db_xref="taxon:7227"
/clone="GH01076"
/clone="GH01076"
/clone="Ib="GH Drosophila melanogaster head pOT2"
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/sex="male and female"
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pOT2. plasmid cDNA library."
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Pred. No. 1.5e-74;
0; Mismatches 234
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                                                                                                                                                                                                      CCCACTACATGATGTTAACCGAACAAACTCGGGGTCTTTTCCATCGTGGTATACTAATGT 730
                                                                                                                                                                                                                                            GTTTCGGCGGAGATCCCAACTGCATCACTGTTTTTGGAGAGAGTGCTGGAGGCGCCTCCA
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                      AGAACGTAAAGGCCAAGGATCTTATTCGCGTGGAGGAAAATGTCCTGACACTGGAGGAAC
                                               TGAAAGCCAAGCCACAGGATTTAATAAAACTTGAGGAAAAAGTTTTAACTCTAGAAGAGC
                                                                                         TAGCCAAATTGGCCGGCTATAAGGGTGAGGATAATGATAAGGATGTTTTGGAATTTCTTA
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AI388926.1
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423 847 363 787 303

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ATCGTGATATGTATGGTCCTGATTATTTCATTAAAAAGGATGTGGTGTTGATTAACATAC 490
                                                                                 ATCGGGAATGGTATGGCCCGGATTACTTTATGAAAGAAGATGTTGTTCTCGTCACGATAC
AGTACCGACTTGGGGCTTTGGGATTTATGAGTCTTAAGTCCCCCGAGCTAAATGTACCAG
                      AATATCGTTTGGGAGCTCTAGGTTTTCTAAGTTTAAATTCAGAAGACCTTAATGTGCCCG 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 649)
Harvey, D., Brokstein, P., Hong, L.,
Lewis, S. and Rubin, G. M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Ins
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilldae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: http://www.fruitfly.org/EST, plate: 199 row: G column: 5
High quality sequence stop: 559.
Location/Qualifiers
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                                                                                                                                                                                                                                                                       /clone="GH19977"
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/sex="male and female"
/sex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
/note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
xhoI; Sized fractionated cDNMs were directly ligated into
pOT2. Plasmid cDNA library."
160 c 172 g 152 t
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/db_xref="taxon:7227"
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Berkeley, CA
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Pred. No. 1.7e-66;
0; Mismatches 210;
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 ATACCGTACGCCCAACCGCCAGTGGGGTGAGCTGAGATTTAAAGCACCCCAGCGACCAACA 240
                                     CAAGTGAGGGGTATCAAGCGTCTATCTCTACGATGTGCCCTACTTCAGCTTCGAGGGT
                                                                      AAAGTGAAAGGCGTTAAACGTTTAACTGTGTACGATGATTCCTACTACAGTTTTTGAGGGGT 180
                                                                                                                             AAGTTTTTAAACTATCGTTTAACTACCAATGAAACGGTGGTAGCTGAAACTGAATATGGC 120
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One Cyclotron Rd, Berkeley, CA
Fax: 510 486 6798
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Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
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/lab_host="DH5 - alpha"
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/note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
XhoI; Sized fractionated cDNAs were directly ligated into
pOT2. Plasmid cDNA library."
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/db_xref="taxon:7227"
/clone="GH23036"
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/sex="male and female"
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Lewis, S. and Rubin, G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
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1 (bases 1 to 671)
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High quality sequence stop: 538
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BDGP/HHMI RH Drosophila EST Project
Unpublished (2001)
Contact: Stapleton, M.
BDGP
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BH14337.5prime RH Drosophila melanogaster normalized Head pFlc-1
BH14337.5prime RH Drosophila melanogaster normalized Head pFlc-1
Drosophila melanogaster CDNA clone RH14337 5 similar to alpha Est7:
Drosophila melanogaster CDNA clone RH14337 5 similar to alpha Est7:
BBan0001112 GO:[carboxyesterase (GO:0004091); carboxyesterase rBan0001112 GO:[carboxyesterase (GO:0004091)] located on: 3R 84D5-84D5;: 08/17/2001, mRNA sequence.
Lawrence Berkeley None Cyclotron Rd, E Fax: 510 486 6798 Email: http://www.f
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Eukaryota; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila
1 (bases 1 to 569)
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                                            Berkeley,
        fruitfly.org/EST,
                                                              National
                                              Lab
, CA
                                                  94720,
              est@fruitfly.berkeley.edu
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Muscomorpha;
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                    GGTAATTCGATACCCACTATGATGGGTAACACTTCATATGAGGGTCTATTTTTCACTTCA
                                                                                                                                                   TTAACTCTAGAAGAGCGTACAAATAAGGTCATGTTTCCTTTTGGTCCCACTGTTGAGCCA
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 AGTAACTCCATCCCCATGTTTATAGGAAACACTTCGTACGAGGGCCTGCTGTGGGTTCCA
                                                                                               TATCAGACCGCTGATTGTGTCTTACCCAAACATCCTCGGGAAATGGTTAAAACTGCTTGG
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                                                                 TTCTCCACGCCCGAATGTGTGATATCCAAGCCTCCAAAGGAGATGATGAAGACCGCCTGG
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Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: http://www.fruitfly.org/EST, Plate: SD.220 row: F column: 7 High quality sequence stop: 546.
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Meoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 660)
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/note="Vector: pOT2; Site_1: EcoRI; Site_2: xh
fractionated cDNAs were directly ligated into
plasmid cDNA library."
170 c 176 g 145 t
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/db_xref="taxon:7227"
/clone="SD22067"
/clone_lib="SD Drosophila melanogas
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Berkeley, CA 94720,
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Pred. No. 2.8e-57;
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AAAGTGAAAGGCGTTAAACGTTTAACTGTGTACGATGATTCCTACTACAGTTTTGAGGGT 180
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                                                                AAAGTCCAGCAGTATCGCCAGTCGACCAATGAAACAGTTGTCGCCGACACGGAGTACGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: http://www.fruitfly.org/EST, Plate: RH.566 row: G column: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 One Cyclotron Rd, Berkeley, Fax: 510 486 6798
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Lawrence Berkeley National Lab
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ,R., Gonzalez,M., Guarin,H., Harris,N., Li,P., Liao,G., Misra,S., Mungall,C.J., Nunoo,J., Pacleb,J., Paragas,V., Park,S., Phouanenavong,S., Wan,K., Yu,C., Lewis,S.E., Celniker,S. and Rubi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, B., Georg
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1 (bases 1 to 674)
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Eukaryota; Metazoa; Arthropoda; Hexapoda;
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                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                    /note="Organ: head; Vector: pFlc1; Site_1: XhOI; Site_2: BamHI; Library was kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library."

170 c 195 g 155 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Drosophila
/db_xref="taxon:7227"
/clone="RH56682"
                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="male and female"
/dev_stage="Adult"
/lab_host="DH5-alpha TonA"
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                                                                                                                                                                                                                                 Score 250; DB 13;
Pred. No. 3.2e-57;
D; Mismatches 196
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era; Muscomorpha;
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676;

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RESULT 8
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676 bp mRNA linear EST 10-SEP-2001 SD16705.5prime SD Drosophila melanogaster Schneider L2 cell culture pOT2 Drosophila melanogaster cDNA clone SD16705 5 similar to alpha-Est7: FBan0001112 GO:[carboxyesterase (GO:0004091); carboxyesterase (GO:0004091)] located on: 3R 84D5-84D5;: 05/18/2001
                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 676)
                                                                                                                                                                                                                                                                                                                                                                                                                          , mRNA sequence.
BI635372
BI635372.1 GI:1
                                                                                                                                                                                                                                                              Unpublished (2001)
Contact: Stapleton, M.
                                                                                                                                                                                                                                                                              Harvey, D., Brokstein, P., Hong, L.,
Lewis, S. and Rubin, G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
                                                                                                                                                                                                              One Cyclotron Rd, Fax: 510 486 6798
                                                                                                                                                                                                                                        Lawrence Berkeley
               155
                                                                                                                                                                     e: SD.167 row: A column: 5 quality sequence stop: 641.
                                                                                                                                                                                    http://www.fruitfly.org/EST,
SD.167 row: A column: 5
               Plasmid
a 173
                                                                         /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="SD16705"
/clone_Lib="SD Drosophila melanogas
culture porz"
culture porz"
                        /note="Vector: pOT2; Sit
fractionated cDNAs were
Plasmid cDNA library."
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                                                             /lab_host="DH5-alpha"
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Berkeley, CA 94720,
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                                                                                        melanogaster
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Local Similarity hes 367; Conserv
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                                                                                                                       Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S., G.M.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Musco
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BI614181.1 GI:155097
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673 bp mRNA linear EST 07-SEP-2001
RH43493.5prime RH Drosophila melanogaster commalized Head pric-1
Drosophila melanogaster cDNA clone RH43493 5 similar to alpha-Est7:
FBan0001112 GO:[carboxyesterase (GO:0004091); carboxyesterase:
(GO:0004091)] located on: 3R 84D5-84D5;: 08/18/2001, mRNA sequence.
                                                                      BDGP/HHMI RH Drosophila
Unpublished (2001)
                                                                                                                                                                                                                                                                                 Ephydroidea; Drosophilidae;
1 (bases 1 to 673)
                                                                                                                                                                                                                                                                                                                                                                                                                      fruit fly.
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Muscomorpha;
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                                                                                                                              AATGTACCAGGAAATGCTGGCCT
                                                                                                                                               AATGTGCCCGGTAATGCCGGCCT
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BI614443 hrangester 572 bp mRNA linear EST 07-SEP-2001 RH43812.5prime RH Drosophila melanogaster normalized Head pF1c-1 Drosophila melanogaster cDNA clone RH43812 5 similar to alpha-Est7: FBan0001112 GO:[carboxyesterase (GO:0004091); carboxyesterase
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/dev_stage="Adult"
/lab_host="DH5-alpha TonA"
/note="Organ: head; Vector: pFlc1; Site_1: XhoI; Site_2:
_bamHI; Library was kindly generated by Piero Carninci at
_the RIKEN. The library was normalized and excised using
_cre_recombinase. Plasmid cDNA library."
_a 169 c 195 g 155 t 1 others
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/db_xref="taxon:7227"
/clone="RH43493"
/clone_lib="RH Drosophila
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                                                                                                                                                CCCTGGGATGGTGCGTGATTGTTGCAATCATAAAGATAAGTCAGTGCAAGTTGATTTT
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                                                        GTCTTCGATAAGGTAGAGGGCTCCGAGGACTGCCTCTATCTCAATGTGTACACCAACAAT
                                                                           ATAACGGGCAAAGTGTGTGTGCCAGAGGATTGTCTATACCTAAGTGTCTATACGAATAAT
                                                                                                                              CCCTGGGAGCGAGTTCGCGACTGCAGCCAGCCGAAGGATAAGGCCGTCCAGGTGCAGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: http://www.fruitfly.org/EST, Plate: RH.438 row: A column: 12
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One Cyclotron Rd, Berkeley, CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BDGP/HHMI RH Drosophila EST Project Unpublished (2001)
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1 (bases 1 to 672)
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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quality sequence stop: 554.
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/lab_host="DH5-alpha TonA"
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pslc-1"
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/db_xref="taxon:7227"
/clone="RH43812"
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  AAGTTTTTAAACTATCGTTTAACTACCAATGAAACGGTGGTAGCTGAAACTGAATATGGC
                                                                                    ATGAATTTCAACGTTAGTTTGATGGAGAAATTAAAATGGAAGATTAAATGCATTGAAAAT
                                                                ATGAATAAGAACCTCGGCTTTGTGGAGCGCTTGCGGTGGCGCCTCAAAACCATCGAGCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarfin, H., Harris, N., Li, P., Liao, G., Misra, S., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and Rubin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       670 bp mRNA linear EST 11-JUL-2001 RE29491.5prime RE Drosophila melanogaster normalized Embryo pFlc-1 Drosophila melanogaster cDNA clone RE29491.5 similar to alpha-Est7: FBan0001112 located on: 3R 84D5-84D5;: 04/12/2001, mRNA sequence. BI233202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lawrence Berkeley National Lab
One cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: RE.394 row: H column: 7
High quality sequence stop: 534.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BDGP/HHMI RE Drosophila EST Project
Unpublished (2001)
Contact: Stapleton, M.
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Eukaryota;
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                                                                                                                                                Conservative
                                                                                                                                                                                                                                       /dev_stage="0-24 hours mixed stage embryonic" .
/lab_host="DH5-alpha TonA"
/note="Organ: embryo; Vector: pFlc1; Site_1: xhoI; Sit
BamHI; Library was kindly generated by Piero Carninci
the RIKEN. The library was normalized and excised usi
Cre recombinase. Plasmid cDNA library."
168 c 194 g 155 t l others
                                                                                                                                                                                                                                                                                                                                                                                                          pFlc-
                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="km22491"
/clone_11b="RE Drosophila melanogaster normalized
                                                                                                                                                                                                                                                                                                                                                                                     /sex="male and female"
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                                                                                                                                                               Score 246.4; DB 13; Length 670; Pred. No. 3.1e-56;
                                                                                                                                            Mismatches
                                                                                                                                            Indels
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                                                                                                                                                                                                                Lawrence Berkeley National Lab one Cyclotron Rd, Berkeley, CA 94720 Fax: 510 486 6798 Email: http://www.fruitfly.org/EST, Plate: 102 row: B column: 1
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AII13763
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GHI0213.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH10213 5prime similar to U51050:
Drosophila melanogaster alpha esterase (aE7) gene, partial cds.
                                                                                                                                                                                                                                                                                                                                                             Lewis, S. and Rubin, G.M. BDGP/HHMI Drosophila EST Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                    High
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                                                                                                                                                                                                                                                                                                                                          Contact: Stapleton, M.
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                                                                                                                                                                                              quality sequence stop: 435
                                                                                               /organism="Drosophila
/db_xref="taxon:7227"
/clone="GH10213"
  /lab_host="DH5 - alpha"
/note="Organ: head; Vec
                  /clone_lib="GH Drosophila
/sex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                              National Lab
Berkeley, CA
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    Vector:
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                                                                              melanogaster
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por2;
Site_1:
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EST 19-APR-2001

529

469

409

349 240

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Site\_2:

.berkeley.edu

Su,C.,

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KEYWORDS
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AUTHORS
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                                                                                                       Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Musco
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                        A1403098 648 bp mRNA linear EST 19-APR-2001 GH22464.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH22464 5prime similar to U51050: Drosophila melanogaster alpha esterase (aE7) gene, partial cds,
                BDGP
                                       BDGP/HHMI Drosophila EST
Unpublished (2001)
                                                                                                                                                                                     EST
                                                                 Harvey,D., Brokstein,P., Hong,L.,
Lewis,S. and Rubin,G.M.
                                                                                                                                                                                                 AI403098.1
 Lawrence
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Pred. No. 7.4e-56;
0; Mismatches 195;
                                                                                 Evans-Holm, M.,
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RESULT 14
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All09901 646 bp mRNA linear EST 19-APR-GH09292.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH09292.5prime similar to U51050: Drosophila melanogaster alpha esterase (aE7) gene, partial cds, mRNA sequence.
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/note="Organ: head; Vector: pOT2;
/note; Sized fractionated cDNAs wer
xho; Sized fractionated cDNAs wer
pOT2. Plasmid cDNA library."
164 c 184 g 149 t
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/sex="male and female"
/dev_stage="adult"
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/db_xref="taxon:7227"
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
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Plate: 92 row: H column: 8
High quality sequence stop: 513.
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Fax: 510 486 6798
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ATTAACATACAATATCGTTTGGGAGCTCTAGGTTTTCTAAGTTTAAATTCAGAAGACCTT
                                                                        GGCGAGGCCAATCGGGAATGGTATGGCCCGGATTACTTTATGAAAGAAGAAGATGTTGTTCTC
                                                                                                     GGTGAAAATCATCGTGATATGTATGGTCCTGATTATTTCATTAAAAAAGGATGTGGTGTTG
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Charlotron Rd, Berkeley, CA 94720, USA
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/db_xref="taxon:7227"
/db_xref="taxon:7227"
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/clone="GH09292"
/clone=lib="GH Drosophila melanogaster head pOT2"
/clone_lib="GH Drosophila melanogaster head pOT2"
/dev_stage="adult"
/dev_stage="adult"
/dev_stage="adult"
/lab_host="DH5 - alpha"
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2e-55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 646)
Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M.
Lewis, S., and Rubin, G.M.
                                                                                                                           AAAGTGAAAGGCGTTAAACGTTTAACTGTGTACGATGATTCCTACTACAGTTTTGAGGGT 180
                                                                                                                                                                           AAGTTTTTAAACTATCGTTTAACTACCAATGAAACGGTGGTAGCTGAAACTGAATATGGC 120
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                                                                                              CAAGTGAGGGGTATCAAGCGTCTATCTCTACGATGTGCCCTACTTCAGCTTCGAGGGT
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                                                 ATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCACCCCAGCGAGCAACA 240
   CCCTGGGATGGTGTGCGTGATTGTTGCAATCATAAAGATAAGTCAGTGCAAGTTGATTTT 300
                                 ATCCCGTACGCCCAGCCTCCGGTGGGGGGGGTTTGCGGTTTAAGGCCCCCTCAGAGGCCCATT 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lawrence Berkeley National Lab
Come Cyclotron Rd, Berkeley, CA 94720,
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/db_xref="taxon:7227"
/clone="LP06524"
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Site_2: Xhol; Sized fractionated cDNAs were
ligated into pOT2. Plasmid cDNA library.
                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="male and female"
/dev_stage="larvae-pupae"
/lab_host="DH5-alpha"
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Best Local Similarity
Matches 1713; Conserv
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patebrin Release #1.0, Vei
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,524
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Price, Robert L.
REGISTRATION NUMBER: 22,685
REFERENCE/DOCKET NUMBER: 1451-021
TELEPHONE: 703-684-1111
TELEPHX: 703-684-1124
THEORMATION FOR STO IT. NO. 1.
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APPLICANT: NEWCOMB, Richard D.
APPLICANT: ROBIN, Geoffrey C.
APPLICANT: BOYCE, Thomas M.
APPLICANT: CAMPELL, Peter M.
APPLICANT: CAMPELL, Poter M.
APPLICANT: OAKESHOTT, John G.
                                                                                                                                                                                                          TELEFAX: 703-684-1124 INFORMATION FOR SEQ ID NO:
                                                                                     TYPE: nucleic
STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE: I
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TITLE OF INVENTION: ENZYME BASED
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lowe Price Leblanc &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1713 base pairs
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CITY: Alexandria
STATE: Virginia
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Y: USA
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   Score 1713;
Pred. No. 0;
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Scoring table:

Title: Perfect score:

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US-09-068-960-7
                                                                                                                   APPLICANT: Commonwealth Scientific and Industrial Rsr
TITLE OF INVENTION: MALATHION CARBOXYLESTERASE
FILE REFERENCE: Attorney Docket No. 6235515 50179-051
CURRENT APPLICATION UNMBER: US/09/068,960A
CURRENT FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER FILING DATE: 1996-11-22
EARLIER APPLICATION NUMBER: AU 6751
EARLIER APPLICATION UNMBER: AU 6751
EARLIER FILING DATE: 1995-11-23
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 1713
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US-09-068-960-7
; Sequence 7, Application
; Patent No. 6235515
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                              AATTGCGCCAACTTTGGTGGCAATCCCCGATAATATTACAGTCTTTTGGTGAAAGTGCCCGGT
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		LENGTH: 1713 TYPE: DNA ORGANISM: Lucilia cuprina 09-068-960-9	LENG TYPE ORGA S-09-06	g
		SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 9	SOFTV SOFTV	
		IER APPLICATION NUMBER: AU 6751 LIER FILING DATE: 1995-11-23	EARL)	
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		REFERENCE: Attorney Docket No. 6235515 50179-051 ENT APPLICATION NUMBERS 52/09/068,960A	CURRE	
		ENERAL INFORMATION: APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org. TITLE OF INVENTION: MALATHION CARBOXYLESTERASE	GENERA APPLI TITLE	
		NS-09-068-960-9 Sequence 9, Application US/09068960A Patent No. 6235515	S-09-06 Sequer	g
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                CAAATGCCTATGCTTGAAGGAATTGGAAACTTGTGTCAATTTTGTGCCAAGTGAATTG
                                     GAAGAGCGTACAAATAAGGTCATGTTTCCTTTTGGTCCCACTGTTGAGCCATATCAGACC
                                                                                    GAAGAGCGTACAAATAAGGTCATGTTTCCTTTTGGTCCCACTGTTGAGCCATATCAGACC
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                                                                                                     TTTCTTATGAAAGCCAAGCCACAGGATTTAATAAAACTTGAGGAAAAAGTTTTAACTCTA
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Sequence 1, Application US/09068960A

Sequence 1, Application US/09068960A

Patent No. 6235515

GENERAL INFORMATION:

APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org

ITITLE OF INVENTION: MALATHION CARBOXYLESTERASE

FILE REFERENCE: Attorney Docket No. 6235515 50179-051

CURRENT APPLICATION UNMBER: US/09/068,960A

CURRENT FILING DATE: 1998-05-20

EARLIER APPLICATION NUMBER: PCT/AU96/00746

EARLIER APPLICATION NUMBER: AU 6751

EARLIER APPLICATION NUMBER: AU 6751

EARLIER FILING DATE: 1995-11-23

NUMBER OF SEQ ID NOS: 43

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1

LENGTH: 1713

TYPE: DNA

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ORGANISM: Lucilia
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                    GCTGATGCTGAACGCACCGCCCCAGAGACCTTGGAAATGGGTGCTAAAATTAAAAAGGCT 1200
                                                                        ATACCCACTATGATGGGTAACACTTCATATGAGGGTCTATTTTTCACTTCAATTCTTAAG
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0;	sdı	y Match 99.3%; Score 1701.8; DB 4; Length 1713; Local Similarity 99.6%; Pred. No. 0; hes 1706; Conservative 0; Mismatches 7; Indels 0; Ga	Query Best I Matche	
		TYPE: DNA ORGANISM: Lucilia cuprina 09-068-960-3	-09	us;
		ID NO 3	SEQ II	
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		IER APPLICATION NUMBER: AU 6751 TER APPLICATION NUMBER: AU 6751	EARL	
		ENT FILING DATE: 1998-05-20 IER APPLICATION NUMBER: PCT/AU96/00746	CURRE	
		FILE REFERENCE: ATTORNY DOCKET NO. 6235515 50179-051 CURRENT APPLICATION NUMBER: US/09/068,960A	FILE	
		ICANT: Commonwealth Scientific and Industrial Rsrch. Org.	APPLI	
		t No. 6235515 aL INFORMATION:	Patent GENER!	
		5 68-960-3 700-3 Prolination HC/000688660x	SULT 5	. US
		81 TCGATGTTTGAAAAACATAGAGATTTATTTTAG 1713	168	Db
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	6	61 ATGGAAAATGTTTCCTGGGATCCAATTAAGAAATCCGATGAAGTATACAAGTGTTTGAAT	15	DЪ
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	1560	01 ACTGGTATATGGATACAATTTGCCACCACTGGTAATCCTTATAGCAATGAAATTGAAGGT	<del>1.1</del>	. Dp
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	1500	41 AATCAATTGGCCAAACGTATGCCTAAAGAATCGCGTGAATACAAAACAATTGAACGTATG	144	Qγ
	1440	81 CGTAGTGGACGTGGTGTTAGGGGTGTTAGTCATGCTGATGAATTAACCTATTTCTTCTGG	138	Db
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	1380	21 GTCTACTTGTATCGCTTCGACTTTGATTCGGAAGATCTTATTAATCCCTATCGTATTATG	132	γo
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Sequence 5, Application US/09068960A

patent No. 6235515

patent No. 6235515

patent No. 6235515

GENERAL INFORMATION:
APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org
APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org
ITLE OF INVENTION: MALATHION CARBOXYLESTERASE
ITLE OF INVENTION INVENTION OF 6235515 50179-051

FILE REFERENCE: Attorney Docket No. 6235515 50179-051

FILE REFERENCE: Attorney Docket No. 6235515 50179-051

FILE REFERENCE: Attorney Docket No. 6235515 50179-051

FILE REFILING DATE: 1996-05-20

CURRENT FILING DATE: 1996-11-23

EARLIER APPLICATION NUMBER: AU 6751

EARLIER APPLICATION NUMBER: AU 6751

EARLIER APPLICATION NUMBER: AU 6751

EARLIER FILING DATE: 1996-11-23

NUMBER OF SEQ ID NOS: 43

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 5

LENGTH: 1713
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                     TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1713 base pairs
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                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,524
FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Price, Robert L.
REGISTRATION UMBER: 22,685
REFERENCE/DOCKET NUMBER: 1451-021
TELECOMMUNICATION INFORMATION:
TELECHONE: 703-684-1111
TELECOMMUNICATION INFORMATION:
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TYPE: nucleic
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ROBIN, Geoffrey C.
BOYCE, Thomas M.
CAMPELL, Peter M.
CAMPELL, Peter M.
PARKER, Anthony G.
OAKESHOTT, John G.
SMYTH, Kerrie A.
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RESULT 8.

US-09-068-960-14

Sequence 14, Application US/09068960A

Patent No. 6235515

GENERAL INFORMATION:

APPLICANT COMMONOWEALTH Scientific and Industrial Rsrch.

TITLE OF INVENTION: MALATHION CARBOXYLESTERASE

FILE REFERENCE: Attorney Docket No. 6235515 50179-051

CUURRENT APPLICATION NUMBER: US/09/068,960A

CURRENT FILING DATE: 1998-05-20

EARLIER APPLICATION NUMBER: PCT/AU96/00746

EARLIER APPLICATION NUMBER: AU 6751

EARLIER FILING DATE: 1995-11-23

NUMBER OF SEQ ID NOS: 43

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 14

LENGTH: 1710

TYPE: DNA

ORGANISM: Musca domestica

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Pred. No. 1.2e-269;
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                                                                                                                                                                                                                                                                                                                        Sequence 51, Application US/08747221B Patent No. 6063610 GENERAL INFORMATION:
        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,221B
FILING DATE: No. 6063610ember 12, 19
CLASSIFICATION: 435
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APPLICANT: Wisnewski,
                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                    TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic TITLE OF INVENTION: Molecules, Proteins and Uses Thereof NUMBER OF SEQUENCES: 66
ATTORNEY/AGENT INFORMATION
                                                                                                                                                   STREET: 1825 Sharp F
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
                                                                                                                                                                                                           ADDRESSEE: Carol Talkington Verser, ADDRESSEE: Heska Corporation
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REGISTRATION NUMBER:

Verser, Carol Talkington RATION NUMBER: 37,459

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; NAME/KEY:
; LOCATION:
US-08-747-221B-51
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Best Local S
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Matches 361;
RESULT 10
US-08-747-221B-52/c
US-08-747-221B-52/c
Sequence 52, Application US/08747221B
Patent No. 6063610
GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
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INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
SEQUENCE 1584 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: FC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 ATGGCAAAGTGAAAGGCGTTAAACGTTTAACTGTGTACGATGATTCCTACAGTTTTG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 AGGGTATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCACCCCAGCGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149 CAGAACCTTGGTCAGGTGTTCTTGATGCTAGTAAAGAAGGGAATAGTTGTAGATCAGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 AAGGTACTTTAAAAGGAAAAGGAAATTAGTGAAAAAGGAAATGTGTTCCATAGTTATT 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89 CTGGAATTCCATATGCCAAACCTCCTGTAGGTGATCTAAGATTTAAGCCACCTCAACCTG 148
                                                                                                                                                                                                                                                                                                                                                                           329
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                                                                                                                                                                                                                                                                                                                                                                                                                               CAAAAACATCAGAAAATCACTTCTTCCAGTAATGGTATGGATACATGGAAGGAGGCTTCT 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTTTATTAAAAAAATTTAAAGTAGGGGGCTGAAGATTGTTTATACCTCAATGTCTATGTAC 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTTATAACGGGCAAAGTGTGTGGCTCAGAGGATTGTCTATACCTAAGTGTCTATĄCGA 355
                                                                                                                                                                                                                                                                                                                                                                          TGTTGATTAACATACAATATCGTTTGGGAGCTCTAGGTTTTCTAAGTTTAAATTCAGAAG
                                                                                                                                                                                                                                                                    AA-----GCGCCTGGCAATGTTGGTTTGATGGACCAGGTTGAAGCTCTAAAATGGGTAA
                                                                                                                                                                                                                                                                                     ACCTTAATGTGCCCGGTAATGCCGGCCTTAAAGATCAAGTCATGGCCTTGCGTTGGATTA 595
                                                                                                                                                                                                                                                                                                                       TTCTGGTTACTTTCAATTATCGATTAGGTGTTTTTGGGATTTTTTGAACCTGGGAATAGAAG
                                                                                                                                                                                                                 GTGGTATACTAATGTCGGGTAATGCTATTTGTCCATGGGC
                                                                                                                                                              CAGGTGGTGCAAGTGTTCATTATTTGATGTTATCAGATCTTTCCAAAGGACTTTTTCATA 622
                                                                                                                                                                            CCGGTGCTGCCTCTACCCACTACATGATGTTAACCGAACAAACTCGCGGTCTTTTCCATC 715
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Verser, Carol Talkington REGISTRATION NUMBER: 37,459 REFERENCE/DOCKET NUMBER: EC-1 TELECOMMUTICATION INFORMATION: TELEPHONE: 970,4493-7272 TELEPAN: 970,444-9505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE 1584 nucleotid
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TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
TITLE OF INVENTION: AR
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BM PC compatible
COMPUTER: Wordperfect for Windows, Version
SOFTWARE: Wordperfect for Windows, Version
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: 1. MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                       1556 AAGGTACTTTAAAAGGAAAAGAAGCAAATTAGTGAAAAAGGAAATGTGTTCCATAGTTATT 1497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Carol Talkington Verser, Ph.D. ADDRESSEE: Heska Corporation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Fort Collins
STATE: Colorado
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                                                                                                                                                                                                                                                                                                                 1436
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FILING DATE: NO. 6063610ember 12, 1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 80525
                                                                                                                                                                                   116 ATGGCAAAGTGAAAGGCGTTAAACGTTTAACTGTGTACGATGATTCCTACTACAGTTTTG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
1136
                                                                                                                                                                                                                                                                                                                                             236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                        416
                                                                                                                                                                                                                                                                     ATTTTATAACGGCAAAGTGTGTGTGGCTCAGAGGATTGTCTATACCTAAGTGTGTCTATACGA 355
                                                                                                                                                                                                                                                                                                             CAGAACCTTGGTCAGGTGTTCTTGATGCTAGTAAAGAAGGGGAATAGTTGTAGATCAGTAC 1377
                                                                                                                                                                                                                                                                                                                                          CAACACCCTGGGATGGTGTGCGTGATTGTTGCAATCATAAAGATAAGTCAGTGCAAGTTG 295
                                                                                                                      TTATCGGTGAAAATCATCGTGATATGTATGGTCCTGATTATTTCATTAAAAAGGATGTGG 475
                                                                                                                                                                                                         ATTTTATTAAAAAAATTAAAGTAGGGGCTGAAGATTGTTTATACCTCAATGTCTATGTAC 1317
                                                                             TGTTGATTAACATACAATATCGTTTGGGAGCTCTAGGTTTTCTAAGTTTAAATTCAGAAG 535
                      ACCTTAATGTGCCCGGTAATGCCGGCCTTAAAGATCAAGTCATGGCCTTGCGTTGGATTA 595
                                                             TTCTGGTTACTTTCAATTATCGATTAGGTGTTTTTGGGGATTTTTGAACCTGGGAATAGAAG
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 -GCGCCTGGCAATGTTGGTTTGATGGACCAGGTTGAAGCTCTAAAATGGGTAA 1083
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Pred. No. 3.8e-43;
0; Mismatches 273;
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US-09-005-051-51
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; LOCATION:
US-09-005-051-51
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                                                                                                                   Query Match 10.0
Best Local Similarity 56.4
Matches 361; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                        NAME: Verser, Carol Talkington
REGISTION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/747,221
FILING DATE: No. 6291222ember 12,
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Silver, Ga
APPLICANT: Wisnewski,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1022
                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1082
                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           716 GTGGTATACTAATGTCGGGTAATGCTATTTGTCCATGGGC 755
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                             176
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 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Carol Talkington Verser, Ph.D. ADDRESSEE: Heska Corporation
                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAAATAATTGCGCCAACTTTGGTGGCAATCCCGATAATATTACAGTCTTTGGTGAAAGTG
               AGGGTATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCACCCCAGCGAC 235
                                                                                    ATGGCAAAGTGAAAGGCGTTAAACGTTTAACTGTGTACGATGATTCCTACTACAGTTTTG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGCGATCTCACAAAGTGGAAGTGCTTTTAATCCTTGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGGTGGTGCAAGTGTTCATTATTTGATGTTATCAGATCTTTCCAAAGGACTTTTTCATA 963
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CTGGAATTCCATATGCCAAACCTCCTGTAGGTGATCTAAGATTTAAGCCACCTCAACCTG 148
                                                        AAGGTACTTTAAAAAGGAAAAGAGCAAATTAGTGAAAAAGGAAATGTGTTCCATAGTTATT
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                                                                                                                                                                                                                                                                                                  1584 nucleotides
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No. 6291222el Carboxylesterase Nucleic
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                                                                                                                 Score 181.2; DB 4;
Pred. No. 3.8e-43;
0; Mismatches 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Version 7.0
                                                                                                                                                DB 4;
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                                                                                                                    Indels
                                                                                                                                                Length 1584;
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US-09-005-051-52/c
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                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       503
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                                                                                                                                                                                                                                                                                 STREET: 1825 Sharp
CITY: Fort Collins
STATE: Colorado
                          NAME: Verser, Carol REGISTRATION NUMBER:
                                                                                                                                 FILING DATE:
                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Carol
ADDRESSEE: Heska
                                                                                                                                                                                                                                                      80525
                                                                                                                                                                                                                                                                   USA
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Sequence 52, Application US/09005051 Patent No. 6291222
                                                                                              APPLICATION NUMBER: 08/747,221 FILING DATE: No. 6291222ember 12, ATTORREY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows,
CURRENT APPLICATION DATA:
REFERENCE/DOCKET NUMBER: FO TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Silver, Gary W. APPLICANT: Wisnewski, Nanc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236 CAACACCCTGGGATGGTGCGTGATTGTTGCAATCATAAAGATAAGTCAGTGCAAGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carol Talkington Verser, Heska Corporation
25 Sharp Point Drive
                                         Carol Talkington
UMBER: 37,459
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STREET: CITY: F STATE:

Fort Collins
Colorado

Drive

COUNTRY:

USA

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RESULT 13
US-08-747-221B-36
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                                                                                           Sequence 36, Application US/08747221B
Patent No. 6063610
GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Wisnewski, Nancy
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-005-051-52
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                                                  TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 970/484-9595
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENCTH: 1584 nucleotid
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                                                                                                                                                                                                                                                                                                                                 CCGGTGCTGCCTCTACCCACTACATGATGTTAACCGAACAAACTCGCGGTCTTTTCCATC
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illarity 56.4%;
Conservative
Carol Talkington Verser, Ph. Heska Corporation
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Pred. No. 3.8e-43;
0; Mismatches 273;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 10.6%;
Best Local Similarity 56.4%;
Matches 361; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO:
             513
                                            596
                                                                           459
                                                                                                                                          399
                                                                                                           536
                                                                                                                                               476 TGTTGATTAACATACAATATCGTTTGGGAGCTCTAGGTTTTCTAAGTTTAAATTCAGAAG
                                                                                                                                                                                                        339
                                                                                                                                                                                                           416 TTATCGGTGAAAATCATCGTGATATGTATGGTCCTGATTATTTCATTAAAAAGGATGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                                                                                                                                      279 CAAAAACATCAGAGAAATCACTTCTTCCAGTAATGGTATGGATACATGGAGGAGGCTTCT 338
                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 2007 nucleotides
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                                                                                                                                                                                                                                                                                                                                   219
                                                                                                                                                                                                                                                                                                                                                                                                  159
                                                                                                                                                                                                                                                                                                                                                                                                                 236 CAACACCCTGGGATGGTGTGCGTGATTGTTGCAATCATAAAGATAAGTCAGTGCAAGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 ATGGCAAAGTGAAAGGCGTTAAACGTTTAACTGTGTACGATGATTCCTACAGTTTTG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39 AAGGTACTTTAAAAGGAAAAGAGCAAATTAGTGAAAAAGGAAATGTGTTCCATAGTTATT 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: No. 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
AAAACAATATTGCATCCTTTGGTGGTGACCCCAACAATGTGACTATTTTTGGAGAATCAG
                             AAAATAATTGCGCCAACTTTGGTGGCAATCCCGATAATATTACAGTCTTTGGTGAAAGTG
                                                             AA-----GCGCCTGGCAATGTTGGTTTGATGGACCAGGTTGAAGCTCTAAAATGGGTAA
                                                                                          ACCTTAATGTGCCCGGTAATGCCGGCCTTAAAGATCAAGTCATGGCCTTGCGTTGGATTA 595
                                                                                                                            TTCTGGTTACTTTCAATTATCGATTAGGTGTTTTGGGATTTTTGAACCTGGGAATAGAAG
                                                                                                                                                                                          TCATGGGATCTGGAAATAGTGATATGGTATGGTCCTGAATATTTGATGGATTATGGAATTG
                                                                                                                                                                                                                                                                                                                                        ATTTTATAACGGGCAAAGTGTGTGTGGCTCAGAGGGATTGTCTATACCTAAGTGTCTATACGA 355
                                                                                                                                                                                                                                                                                                                                                                                   CAGAACCTTGGTCAGGTGTTCTTGATGCTAGTAAAGAAGGGGAATAGTTGTAGATCAGTAC
                                                                                                                                                                                                                                                                                                                     ATTTTATTAAAAAAATTAAAGTAGGGGCTGAAGATTGTTTATACCTCAATGTCTATGTAC 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Verser, Carol Talkington REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEPHONE: 970/493-7272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Wordberfect for Windows, Version CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                       1969
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
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                                       1789
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TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
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APPLICANT: Wisnewski,
                                                                                                                                                                                                                    176
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ADDRESSEE: Heska Corporation
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                                   ATTTTATTAAAAAAATTAAAGTAGGGGCTGAAGATTGTTTATACCTCAATGTCTATGTAC
                                                                     ATTTTATAACGGGCAAAGTGTGTGGCTCAGAGGATTGTCTATACCTAAGTGTCTATACGA 355
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Pred. No. 4.3e-43;
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Patent No. 6291222
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                                                                                                                 TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO:
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                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 2007 nucleotides
                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/747,221 FILING DATE: NO. 6291222ember ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US
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MEDIUM TYPE: Floppy
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MOLECULE
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APPLICANT: Wisnewski,
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CITY: Fort Collins
                  TOPOLOGY:
                                                                                                                                                                                                              NAME: Verser, Carol Talkington REGISTRATION NUMBER: 37,459
                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: Windows 95 SOFTWARE: WordPerfect for Windows,
                                    STRANDEDNESS:
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                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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  TYPE:
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No. 6291222el Carboxylesterase Nucleic Acid
Molecules, Proteins and Uses Thereof
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Search completed: April 11, 2003, 08:51:28 Job time : 46.5118 secs
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                                                             633 AAGCGATCTCACAAAGTGGAAGTGCTTTTAATCCTTGGGC 672
                            716 GTGGTATACTAATGTCGGGTAATGCTATTTGTCCATGGGC 755
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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
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      US-09-776-910-7
1713
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Listing first 45 summaries
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                                                                                                                                                                                                                 /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
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15895.765 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result	Score	Query Match	Length	DВ	ID	Description
ь	87.2	5.1	1691	ٔ و	US-10-083-590-13	Sequence 13, Appl
N	77.2	4.5	1611	9	US-09-738-626-1254	125
ω	62.2	3.6	1967	10	US-09-748-739A-1	Sequence 1, Appli
4	62.2		2381	10	US-09-880-107-2271	Sequence 2271, Ap
<sub>5</sub>	62.2		2416	10	US-09-748-739A-3	Sequence 3, Appli
6	62.2		2416	10	US-09-748-739A-5	Sequence 5, Appli
7	62.2		2416	10	US-09-748-739A-7	<ul> <li>Sequence 7, Appli</li> </ul>
8	62.2		2416	10	US-09-748-739A-16	16,
9	62.2		2444	9	US-09-893-519A-112	Sequence 112, App
10	59		2508	10	US-09-934-323-3	
11	59		4667	10	US-09-934-323-1	Sequence 1, Appli
12	57.8		657	10	US-09-974-300-1107	Sequence 1107, Ap
13	57		2428	9	US-09-418-176-1	Sequence 1, Appli
14	57		2428	10	US-09-969-347-220	Sequence 220, App
15	56.8	3 3	2191	9	US-09-954-531-1038	Sequence 1038, Ap
16	56.8	3.3	2191	10	US-09-880-107-3854	Sequence 3854, Ap
17	56.8		2484	9	US-10-102-806-271	Sequence 271, App
18	56.4	3.3	2451	9	US-09-875-353-3	Sequence 3, Appli
19	56.4	ω . ω	3502	9	US-09-875-353-1	Sequence 1, Appli

55.4 3.2 2087 10 US-09-89-860-1 55.4 3.2 3824 9 US-10-036-041-22 55.4 3.2 3824 9 US-10-028-072-541 55.4 3.2 3824 9 US-10-028-072-541 55.4 3.2 3824 9 US-10-121-049-541 55.4 3.2 3824 9 US-10-127-049-541 55.4 3.2 3824 9 US-10-176-918-62 55.4 3.2 3824 9 US-10-176-918-641 55.4 3.2 3824 9 US-10-176-918-641 55.4 3.2 3824 9 US-10-176-918-641 55.4 3.2 3824 9 US-10-176-918-64-20 55.4 3.2 3824 9 US-10-176-918-65-641 55.4 3.2 3824 9 US-10-36-21-42 55.4 3.2 3824 9 US-10-36-21-42 55.4 3.2 3824 9 US-10-137-865-541 55.4 3.2 3824 9 US-10-137-865-641 55.4 3.2 3824 9 US-10-142-431-541 55.4 3.2 3824 9 US-10-142-431-541 55.4 3.2 3824 9 US-10-143-114-541 55.4 3.2 3824 9 US-10-143-143-150 55.4 3.2 3824 9 US-10-136-160-22 55.4 3.2 3824 9 US-10-305-308-209 55.4 3.2 3824 9 US-10-305-308-209
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10 US-09-895-866 10 US-10-036-041 9 US-10-038-072 9 US-10-035-855 9 US-10-121-049 9 US-10-121-049 9 US-10-175-746 9 US-10-176-921
US-09-095-860 US-10-028-072-11-028-072-12-049-075-12-049-075-075-075-075-075-075-075-075-075-075
S-09-895-866 -10-036-071 -10-035-855 -10-121-049 -10-121-049 -10-121-049 -10-176-931-836 -10-176-931-836 -10-176-921 -10-27-884 -10-36-214 -10-35-218 -10-142-431 -10-142-431 -10-142-431 -10-142-431 -10-143-1144 -10-143-1146 -10-142-431 -10-143-1146 -10-142-431 -10-143-1146 -10-230-338

## ALIGNMENTS

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RESULT 1
US-10-083-590-13
; Sequence 13, Application US/10083590
; Publication US20030027257A1
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; TYPE: DNA
; ORGANISM: Heliothis virescens
US-10-083-590-13
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Best Local Similarity 53.3%;
Matches 210; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/083,590
CURRENT FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER:
PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-24
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER:
PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-20
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER:
PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-21
NUMBER: OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: SEQUENCES FOR IMPROVING THE EFFICIENCY OF SECRETION OF TITLE OF INVENTION: NON-SECRETED PROTEINS FROM MAMMALIAN AND INSECT CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 028722-207
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APPLICANT: FARRELL, Patr
                                                                                                                   428 ATCATCGTGATATGTATGGTCCTGATTATTTCATTAAAAAGGGATGTGGGTGTTGATTAACA 487
                                                                                                                                                                                                                  368 CCGAAACTAAACGTCCCGTTTTAGTATACATACATGGTGGTGGTTTTATTATCGGTGAAA 427
500
                                          488 TACAATATCGTTTGGGAGCTCTAGGTTTTCTAAGTTTAAATTCAGAAGACCTTAATGTGC 547
                                                                                                                                                                                         380 CCACACCTTTACGGCCTATCCTGGTGTTCATACATGGTGGAGGATTTGCTTTCGGCTCCG 439
TTAATTACAGATTGAACGTCTTCGGTTTCCTGTCCATGAACACAACA-----AAAATCC
                                                                                            GCCACGAGGACCTACACGGACCAGAATATTTGGTCACTAAGAATGTCATCGTCATCACGT 499
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Pred. No. 1.4e-12;
0; Mismatches 178;
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; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1254
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APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
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                                                                                                                                                                                                                                                                                                                                                Query Match 4.5%;
Best Local Similarity 50.2%;
Matches 277; Conservative
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SEQ ID NO 1254
LENGTH: 1611
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APPLICANT:
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                                                        258
                                                                                                                                                                                                                       237 AACACCCTGGGATGGTGTGCTGATTGTTGCA---ATCATAAAGATAAGTCAGTGCAAGT
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TATTATCGGTGA---AAATCATCGTGATATGTATGGTCCTGATTATTTCATTAAAAAAGGA
                                                                                                                                                              TGATTTTATAACGGGCAAAGTGTGTGGCTCAGAGGATTGTCTATACCTAAGTGTCTATAC
                                                                                          CAAGAAATGGGACGGCGTGCGCGATTGCTCAATGTTCGGTGAAGTAGCTTCTCAGCCAAC
                                                                                                                                                                                                                                                                          GGGAATTCCCTACGGCCGAAACACTGGCGGAAAAATATCGCTTCCGGGCACCCCGGCCCGC
                                                        G-----CCTGATTCCGAAGAAAAGCTTCCTGTTGTGGTGTATCTCCACGGCGGTTCCTT
                                                                                                                              GTACTCCTGGACAGATAAGATTCGCGGTTCAGAAGACTGCCTTAACCTCGATGTCGTGCG
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Pred. No. 5.5e-10;
0; Mismatches 263;
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; LOCATION: (86)...(1891)
US-09-748-739A-1
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                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 190; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lockridge, Oksana
APPLICANT: Watkins, Jeffry D.
TITLE OF INVENTION: Butyrylcholinesterase Variants
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: P-IX 4143
CURRENT APPLICATION NUMBER: US/09/748,739A
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1967
TYPE: DNA
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 622 AATCCCGATAATATTACAGTCTTTGGTGAAAGTGCCGGTGCTGCCTC
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                                                                                                                           GGAGCTCTAGGTTTTCTAAGTTTAAATTCAGAAGACCTTAATGTGCCCGGTAATGCCGGC 561
                                                                                                                                                                          GATGGCAAGTTTCTGGCTCGGGTTGAAAGAGTTATTGTAGTGTCAATGAACTATAGGGTG
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                                                                                                                                                                                                                                                                                                                                     GAGGATTGTCTATACCTAAGTGTCTATACGAATAATCTAAATCCCGAAACTAAACGTCCC 384
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                                                                                                       GGTGCCCTAGGATTCTTAGCTTT----GCCAGGAAATCCTGAGGCTCCAGGGAACATGGGT
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                                      TTATTTGATCAACAGTTGGCTCTTCAGTGGGTTCAAAAAAATATAGCAGCCTTTGGTGGA
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Pred. No. 5e-06;
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; OTHER INFORMATION: Genbank Accession No. US20020142981A1 M16474
US-09-880-107-2271
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                                                                                                                                              GENERAL INFORMATION:
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Best Local Similarity 54.8%;
Matches 190; Conservative
                                                                                                                                                             Sequence 3, Application US/09748739A Patent No. US20020119489A1
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APPLICANT: Lockridge, Oksana
APPLICANT: Watkins, Jeffry D.
TITLE OF INVENTION: Butyrylcholinesterase '
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: P-IX 4143
CURRENT APPLICATION NUMBER: US/09/748,739A
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/237,054 PRIOR FILING DATE: 2000-10-02 NUMBER OF SEQ ID NOS: 3950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/211,379 PRIOR FILING DATE: 2000-06-14
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TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                        TTATTTGATCAACAGTTGGCTCTTCAGTGGGTTCAAAAAATATAGCAGCCTTTGGTGGA
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Scherf, Uwe
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Pred. No. 5.5e-06;
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                                                                                          Variants
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; NAME/KEY: CDS;
; LOCATION: (214)...(1935)
US-09-748-739A-5
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US-09-748-739A-5
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                                                                                                                                                                                                                                                                                                                            SEQ ID NO 5
LENGTH: 2416
TYPE: DNA
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APPLICANT: Lockridge, Oksana
APPLICANT: Watkins, Jeffry I
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Best Local Similarity
Matches 190; Conserv
                                                                                 Query Match 3.6
Best Local Similarity 54.8
Matches 190; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Watkins, Jeffry D.
TITLE OF INVENTION: Butyrylcholinesterase Variants
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: P-IX 4143
                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/748,739A CURRENT FILING DATE: 2000-12-06 NUMBER OF SEQ ID NOS: 31
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                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 4.0
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NAME/KEY: CDS
LOCATION: (214)...(1935)
                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                           FEATURE:
OTHER INFORMATION: Human
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
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                                         325 GAGGATTGTCTATACCTAAGTGTCTATACGAATAATCTAAATCCCGAAACTAAACGTCCC 384
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GAAGACTGTTTATATCTAAATGTATGGATTCCAGCACCTAAACC---AAAAAATGCCACT 537
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Pred. No. 5.6e-06;
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Pred. No. 5.6e-06;
                                                                                   Mismatches 148;
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Length 2416;

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US-09-748-739A-7

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; NAME/KEY: CDS
; LOCATION: (214)...(1935)
US-09-748-739A-7
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CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: LOCKRIDGE, OKSANA
APPLICANT: Watkins, Jeffry D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/09748739A Patent No. US20020119489A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Butyrylcholinesterase Variants TITLE OF INVENTION: Methods of Use FILE REFERENCE: P-IX 4143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Human
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                                                                                                                                                                                                                                                                                                                                 GAAGACTGTTTATATCTAAATGTATGGATTCCAGCACCTAAACC---AAAAAATGCCACT 537
                                                                                                                                                                                                                                                                                  GTTTTAGTATACATACATGGTGGTGGTGTTTATTATCGGTGAAAATCATCGTGATATGTAT 444
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                                                                                                                                                                                                                                                              GTATTGATATGGATGTTGGTGGTTTTCAAACTGGAACATCATCTTTACATGTTTAT
                                                                                                                                                       GGAGCTCTAGGTTTTCTAAGTTTAAATTCAGAAGACCTTAATGTGCCCGGTAATGCCGGC
                                                    TTATTTGATCAACAGTTGGCTCTTCAGTGGGTTCAAAAAAATATAGCAGCCTTTGGTGGA
                                                                                     CTTAAAGATCAAGTCATGGCCTTGCGTTGGATTAAAAATAATTGCGCCAACTTTGGTGGC 621
                                                                                                                       GGTGCCCTAGGATTCTTAGCTTT----GCCAGGAAATCCTGAGGCTCCAGGGAACATGGGT 714
AATCCCGATAATATTACAGTCTTTGGTGAAAGTGCCGGTGCTGCCTC 668
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milarity 54.8%;
Conservative
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pred. No. 5.6e-06;
0; Mismatches 148;
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US-09-748-739A-16
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SEQ ID NO 16
LENGTH: 2416
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16, Application US/09748739A Patent No. US20020119489A1
                                                                                                                                                                                                                                                                                                                           US-09-893-519A-112
; Sequence 112, Application US/09893519A
; Publication No. US20030027243A1
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APPLICANT: Watkins, Jeffry D.
APPLICANT: Watkins, Jeffry D.
TITLE OF INVENTION: Butyrylcholinesterase Variants
TITLE OF INVENTION: Methods of Use
TITLE REFERENCE: P-IX 4143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/748,739A CURRENT FILING DATE: 2000-12-06
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Best Local Similarity 54.8%;
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                                                                                                                                                                                                                      APPLICANT: APPLICANT:
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                                                                                                                                                                                                                                                                       APPLICANT: ANADYS PHARMACEUTICALS, INC
APPLICANT: THOMPSON, Craig
                                                                                                                                                                                                         APPLICANT:
                                                             APPLICANT:
                                                                                  APPLICANT:
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                                                                                                                                BRADLEY, John
DESILVA, Thamara
HARRIS, Sandra
KOMARNITSKY, Svetlana
MENDILLO, Marc
MCNORE, Daniel
                                                                                                                                                                                                                                                        MOORE, Jeffrey
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                                                                                                                                                                                                                                           BUURMAN, Ed T.
                                                                                                      SANDERSON, Karen
                                                                                                                       MCCOY, Melissa
                                   DAVIDOV,
                                                      LONG,
                                                                     Shuhao
                                                                                     Tariq
                                     Eugene
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Pred. No. 5.6e-06;
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Query Match Best Local S Matches 190

Local Similarity es 190; Conserv

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FEATURE:

FEATURE:

LENGTH:

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; TYPE: DNA
; ORGANISM: HOMO
US-09-934-323-3
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                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09934323 Patent No. US20020150910A1 GENERAL INFORMATION:
    Query Match
Best Local Similarity
Matches 125; Conserv
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Best Local :
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                                                                                                                                                                   SEQ ID NO 3
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TYPE: DNA
ORGANISM: Homo sapiens
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Human Genbank/NM_000055
DATABASE ENTRY DATE: 2001-02-03
RELEVANT RESIDUES: (1)..(2444)
                                                                                                                                                                                PRIOR FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/934,323
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/226,774
                                                                                                                                                                                                                                                                                                            APPLICANT: CUITIS, ROIY A. J.
TITLE OF INVENTION: 33410, A NOVEL HUMAN CARBOXYLESTERASE
TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
FILE REFERENCE: 10448-081001
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PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 60/224,457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: ANTIFUNGAL COMPOUNDS AND METHODS OF USE FILE REFERENCE: 0342/IG548-US2
CURRENT APPLICATION NUMBER: US/09/893,519A
CURRENT FILING DATE: 2001-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 146
                                                                                                                                            LENGTH: 2508
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Similarity 54.8%;
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    Conservative
                       3.4%;
Score 59; DB 1
Pred. No. 3.9e.
0; Mismatches
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Pred. No. 5.6e-06;
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                       DB 10;
3.9e-05;
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, NAME/KEY: CDS
; LOCATION: (420)...(2924)
US-09-934-323-1
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APPLICANY: CUITLIS, ROTY A. J.
TITLE OF INVENTION: 33410, A NOVEL HUMAN CAP
TITLE OF INVENTION: FAMILY MEMBER AND USES
FILE REFERENCE: 10448-081001
                                                         GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Gr
                                                                                                                      Sequence 1107, Application US/09974300 Patent No. US20020146721A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version SEQ ID NO 1 \,
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Patent No. US20020150910A1
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Best Local :
                APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
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  FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 8
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ION: Expression 10085.500-US
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Pred. No. 5.5e
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 1107
LENGTH: 657
TYPE: DNA
ORGANISM: Bacillus licheniformis
US-09-974-300-1107
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Best Local Similarity 49.9%;
Matches 174; Conservative
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PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09418176 Publication No. US20030040040A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION
                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              434 GTGATATGTATGGTCCTGATTATTTCATTAAAAAGGATGTGGTGTTGATTAACATACAAT 493
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                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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                                                                    PRIOR APPLICATION DATA:
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                                                                                      FILING DATE:
CLASSIFICATION:
             APPLICATION NUMBER: 08/6 FILING DATE: 04-APR-1996 NIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                           STATE:
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                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                      COUNTRY: United States ZIP: 10036-2787
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PCT/SE96/00318
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TELEFAX: (212) 354-81 INFORMATION FOR SEQ ID NO:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9:
FILING DATE: 24-MAY-1995
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ATTORNEY/AGENT INFORMATION:
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LOCATION: 82..2319
OTHER INFORMATION: OTHER INFORMATION:
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                                                        Sequence 220, Application US/09969347
Patent No. US20020115085A1
GENERAL INFORMATION:
APPLICANT: Ebner, Reinhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 3.3%;
Best Local Similarity 53.3%;
Matches 120; Conservative
    TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-69
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TAGES: 543-550
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NATE: Sept.-1990
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cDNA cloning of human-milk

bile-salt-stimulated lipase and evidence for its

identity to pancreatic carboxylic ester hydrolase
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Carlsson, Peter
Enerback, Sven
Hernell, Olle
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US-09-954-531-1038
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LENGTH: 2428
TYPE: DNA
                                                                                                          Query Match
Best Local Similarity
Matches 215; Conserv
                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.0 SEQ ID NO 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Weaver, Zoe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1038, Application US/09954531 Patent No. US20020165180A1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C TITLE OF INVENTION: Gene Sets FILE REFERENCE: 68929-77 CURRENT APPLICATION NUMBER: US/09/954,531 CURRENT FILING DATE: 2002-05-02 PRIOR APPLICATION NUMBER: US/02/33,133 PRIOR FILING DATE: US/00-09-18
                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US/60/234,009
PRIOR EILING DATE: 2000-09-20
PRIOR EPILICATION NUMBER: US/60/234,034
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,509
PRIOR PILING DATE: 2000-09-22
PRIOR PILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US/60/234,567
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CURRENT FILLING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US/60/237,598
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US/60/237,604
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 318
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Pred. No. 0.0001
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PI Boyce TM, Campbell PM, Newcomb RD, Oakeshott JG; PI Parker AG, Robin GC, Russell RJ, Smyth K;  XX  DR WPI; 1995-263870/34.  DR N-PSDB; AAQ91561.  XX  PT Pure E3 esterase from Lucilia cuprina and related DNA - used to PT eliminate residues of organo:phosphate and carbamate pesticides from	9440-A1. L-1995. N-1995; 95WO-AU00016. N-1994; 94AU-0003347. ) COMMONWEALTH SCI & IND RES ORG.	SULT 1 R78142 sta AAR78142; AAR78142; 22-DEC-1995 OP-sensitive Esterase; E3 insecticide;	12 1295.5 42.4 565 22 ABB57790 13 1238 40.3 542 22 ABB57790 14 1228.5 40.0 530 22 ABB57790 15 1184 38.5 602 23 AAM47598 16 1073 34.9 551 22 ABB57788 17 1022.5 33.3 541 22 ABB57788 18 955.5 31.1 568 22 ABB57789 19 856 27.9 528 19 AAM57862 20 866 27.5 531 19 AAM57863 21 84.6 27.5 531 19 AAM57863 22 785.5 25.6 530 19 AAM57863 23 785.5 25.6 530 19 AAM57863 24 785.5 25.6 530 19 AAM57863 25 785.5 25.6 530 19 AAM57863 26 785.5 25.6 550 19 AAM57863 27 786.5 25.6 550 19 AAM57863 28 779.5 25.4 550 19 AAM57863 29 779.5 25.4 550 19 AAM57863 30 779.5 25.4 550 19 AAM57863 31 771.5 25.1 505 19 AAM57863 31 771.5 25.1 505 19 AAM57863 32 771.5 25.1 505 29 AAB52931 33 771.5 25.1 505 29 AAB52933 34 754.5 24.6 530 19 AAM57863 35 759.5 24.7 495 19 AAM57863 36 757.5 24.7 562 22 AAB2293 37 754.5 24.6 530 19 AAM57866 38 754.5 24.6 530 19 AAM57866 39 71.5 23.1 505 29 AAB57863 40 71.5 23.1 505 29 AAB57863 40 71.5 23.1 505 29 AAB57863 40 71.5 23.2 575 23 ABB64788 40 71.5 23.2 575 23 ABB64788 40 71.5 23.2 575 23 ABB79538 41 623 20.3 570 19 AAM57860 42 623 20.3 570 22 AAB2293 43 623 20.3 570 22 AAB2293 44 623 20.3 595 19 AAM57860 45 623 20.3 595 19 AAM57860 46 623 20.3 595 19 AAM57860 46 623 20.3 595 19 AAM57860 47 624 625 625 625 625 625 625 625 625 625 625

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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Page 12-17; 38pp; English
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                              Malathion opesticide;
                                                                                     AAW17765;
                                                                                                    AAW17765 standard;
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Key
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                Lucilia
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                                                                                                                                                                       NOLAKRMPKESREYKTIERMTGIWIQFATTGNPYSNEIEGMENVSWDPIKKSDEVYKCIN 540
                                                                                                                                          ISDELKMIDVPEMDKIKQWESMFEKHRDLF 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                 cuprinia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    570 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                               carboxylesterase; organophosphate;
; remediation; bioremediation; decor
                                                      malathion susceptible clone Lc743 esterase
                                                                      (first entry)
   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                      Protein; 570 AA
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                                    decontamination;
                                             insecticide;
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Newcomb RD,
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                                                                                                                                                                                                                                                                                                                                        Esterase E3 (AAW17765) from a malathion susceptible strain of Lucilia cuprinia differs from an esterase enzyme (see also AAW17768) from malathion resistant RMB strains by a Trp for Leu substn. at amino acid position 251, owing to a mutation in the encoding DNA sequence (see also AAT68596). The resistant enzyme, termed malathion carboxylesterase, can be formulated for use in degrading environmental carboxylester or dimethyl general
                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding enzyme that degrades organophosphate useful for decontamination of soil, water, food et
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CSIR ) COMMONWEALTH SCI & IND RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 1; 52pp; English.
                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                organophosphates.
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                                                                                                                                                                                                                  IPYAQPPVGELREKAPQRPTPWDGVRDCCNHKDKSVQVDFITGKVCGSEDCLYLSVYTNN 120
                                                                                                                                                  LNPETKRPVLYXIHGGGFIIGENHRDMYGPDYFIKKDVVLINIQYRLGALGFLSLNSEDL 180
                                                                                                                LNPETKRPVLVYIHGGGFIIGENHRDMYGPDYFIKKDVVLINIQYRLGALGFLSLNSEDL
                                                                                EWFPMHRLLQLRENHTSGTPVYLYRFDFDSEDLINPYRIMRSGRGVKGVSHADELTYFFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT68596.
NQLAKRMPKESREYKTIERMTGIWIQFATTGNPYSNEIEGMENVSWDPIKKSDEVYKCLN
                                                                                                                                                                                                                                                                                          Similarity
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D, Oakeshott JG,
                                                                                                                                                                                                                                                                                                                    570 AA;
                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                            100.0%; Score 3073; DB 18; 100.0%; Pred. No. 7.8e-306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "amino acid
mutants "
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JG, Robin GC,
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RESULT 3
AAW17766
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                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                     Sequence
                                                                                                                                                                              A malathion carboxylesterase (AAW17766) differs from the es (AAW17765) of a malathion susceptible clone of Lucilla cupr a substn. of the tryptophan residue at amino acid position The enzyme is capable of hydrolysing carboxylester and/or dimethyloxon organophosphates and can be formulated for use
                                                                                                                                                                                                                                                                     DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
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                                                                                                                                                                         bioremediation
                                                                                                                                                                                                                                                            useful
                                                                                                                                                                                                                                                                                                           Newcomb
                                                                                                                                                                                                                                                                                                                                       (CSIR )
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pesticide; remediation; bioremediation; decontamination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-AUG-1997
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 121
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                                                                                                                           Loca1
                                                                           Н
                                                                                                                                                                                                                                                         encoding enzyme that degrades organophosphate pesticides ful for decontamination of soil, water, food etc
                                                                        MNFNVSLMEKLKWKIKCIENKFLNYRLTINETVVÅETEYGKVKGVKRLTVYDDSYYSFEG
LNPETKRPVLVYIHGGGFIIGENHRDMYGPDYFIKKDVVLINIQYRLGALGFLSLNSEDL
         LNPETKRPVLVYIHGGGFIIGENHRDMYGPDYFIKKDVVLINIQYRLGALGFLSLNSEDL
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                                             IPYAQPPVGELREKAPQRPTPWDGVRDCCNHKDKSVQVDFITGKVCGSEDCLYLSVYTNN
                                                                                                                  569;
                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                          RD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cuprina.
                                                                                                                                                                                                                                        Fig 1; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; Protein;
                                                                                                                                                                                                                                                                                                                   Brownlie
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                                                                                                                                                                        strategies for
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/note= "pref.
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JC,
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                                                                                                                        99.6%;
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JG, Robin GC,
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. Leu or Ser"
                                                                                                              Score 3060; DB 18;
Pred. No. 1.7e-304;
D; Mismatches 1;
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tion 251.
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180
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RESULT 4
AAW17768
A malathion carboxylesterase (AAW17768), designated RM-8Con, different from the esterase (AAW17765) of a malathion susceptible clone of Lucilla cuprina by a substr. of the tryptophan residue at amino acid position 251 by a leucine residue. This mutation is situated at the base of the active site gorge, 6.5 Angstroms from the active site serine. The RM8Con amino acid sequence is a consensus deduced from the DNA sequences of 3 resistant clones (RM8 A-C) and their
                                                                                                                                                                                                                                     Boyce T,
Newcomb
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                                                                                                                            Claim
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Oakeshott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     carboxylesterase;
                                                                                                                                                           decontamination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       remediation;
                                                                                                                            <u>ب</u>
                                                                                                                                                                      enzyme
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bioremediation; decontamination;
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Russell RJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                   Malathion opesticide;
                                                                Musca
                                                                                                               Md-alpha-E7
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W09719176-A1
                                      Misc-difference
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                                                                 domestica
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                                                                                              carboxylesterase;
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ilarity 99.8%;
Conservative
                                                                                     remediation;
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                                    Location/Qualifiers
251
                                                                 Rutgers
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                    "Ser-251 is tryptophan in the allele expression product"
                                                                                    ase; organophosphate;
bioremediation; decor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 3060; D; Pred. No. 1.7e 0; Mismatches
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l.7e-304;
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Matches 424;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A polypeptide (AAW17767) is the expression product of a mala resistant allele of the Musca domestica Md-alpha-E7 gene, at contains a Ser for Trp substn. at amino acid position 251. enzyme is capable of hydrolysing carboxylester and/or dimethyloxon organophosphates and can be formulated for use in bioremediation strategies for treatment of soil or water
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scontamination of soil, water, food etc
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JG, Robin GC,
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Pred. No. 4.1e-231;
1; Mismatches 75;
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Russell RJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          specification,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid
genes from Drosophila and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence data for this patent did not form cification, but was obtained in electronic :
                                                                                                                                                                                                                                                                                                                                                              MNENVSLMEKLKWKIKCIENKFLNYRLTTNETTVVÆETEYGKVKGVKRLTVYDDSYYSFEG
ILMSGNAICPWA-NTQCQHRAFTLAKLAGYKGEDNDKDVLEFLMKAKPQDLIKLEEKVLT
                                                                        NVPGNAGLKDQVMALRWIKNNCANFGGNPDNITVFGESAGAASTHYMMLTEQTRGLFHRG
                                                                                                                                           VKPDKARPVMVWIHGGGFIIGEANREWYGPDYFMKEDVVLVTIQYRLGALGFMSLKSPEL
                                                                                                                                                                                            LNPETKRPVLVYIHGGGFIIGENHRDMYGPDYFIKKDVVLINIQYRLGALGFLSLNSEDL
                                                                                                                                                                                                                                                                  IPYAQPPVGELREKAPQRPTPWDGVRDCCNHKDKSVQVDFITGKVCGSEDCLYLSVYTNN 120
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)B; ABL01953.
                                               NVPGNAGLKDQVLALKWIKNNCASFGGDPNCITVFGESAGGASTHYMMLTDQTQGLFHRG
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                                 useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLJ6176-ABLJ9511), expressed DNA (ABB5737-ABB72072).
       The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                     Disclosure; SEQ ID NO 363; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB57857 standard; Protein;
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)B; ABL01960.
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11-JUL-2000;
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D5; Mismatches 164; Indels
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                                                                                              PDLKKLMVWESFFRR
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                                                                                                                                                                    KCIERLVGLWTHFAACGNPNFDPEQEDL--
                                                                                                                                                                                                                                                                                                                    IEL-NMDRESALCREYGDQLRQCYYGDKTPSLDTLHEYLQMVSHEYFWFPIYRTVLSRLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure;
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                                                                                                                           capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                           The sequence data for this patent did not form specification, but was obtained in electronic at ftp.wipo.int/pub/published_pct_sequences.
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11-JUL-2000; 2000US-0614150.
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WPI; 2001-656860/75.
N-PSDB; ABL06086.
                                                              Venter JC, Adams M,
                                                                                                    (PEKE ) PE
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New isolated nucleic acid detection reagent for detecting genes from Drosophila and for elucidating cell signalling interactions .
Disclosure; SEQ ID
    NO 12741; 21pp + Sequence Listing; English.
                                                                                         1000 or more
and cell-cell
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discoloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins The invention and žs

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published\_pct\_sequences. WIPO

Sequence 566 AA;

Matches 260; Query Match Best Local S Similarity Conservative 104; Mismatches 42.48; Score 1302.5; DB pred. No. 4e-124; DB 22; 190; Indels Length 19; Gaps 11;

ABB57746;

26-MAR-2002

(first

entry)

ABB57746 standard;

Protein; 565

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Best Local S
Matches 265
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DB; ABL01849.
LKQMPMLVKELETCVNFVPSELADAERTAPETLEMGAKIKKAHVTGETPTADNFMDL---
                           QEERRQYVLFPFTPVVEPYITRDCVLPRCHREMLPEAWGNDLPLILGGNSFEGLFSYQST
                                                   LEERTNKVMFPFGPTVEPYQTADCVLPKHPREMVKTAWGNSIPTMMGNTSYEGLF-FTSI
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Query Match Best Local Matches

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Conservative

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Score 1238; D Pred. No. 1.6e 93; Mismatches

DB 22; l.6e-117; les 177;

Length Indels

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Similarity

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RESULT 13
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                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLJ6176-ABLJ0511) expressed DNA sequences (ABLJ01840-ABLJ6175) and the encoded proteins
                                                                                   (ABB57737-ABB72072)
The sequence data f specification, but
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                                                          at ftp.wipo.int/pub/published_pct_sequences.
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N-PSDB; ABL01893.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            capable of detecting 1000 or more genes from Drosophila. The inventious useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLG1840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IVTVAYRLGALGFLSLDDPQLNVPGNAGLKDQIMALRWVQQNIEAFGGDSNNITLFGESA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MFFRKYAGSEDCLYLNVYVKDLQPDKLRPVMVWIYGGGYQVGEASRDMYSPDFFMSKDVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FITGKVCGSEDCLYLSVYTNNLNPETKRPVLVYIHGGGFIIGENHRDMYGPDYFIKKDVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GPVRGVKRNTIWGGSYFSFEKIPFAKPPVGDLRFKAPEAVEPWDQELDCTSPADKPLQTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGASTHFLALSPQTEGLIHKAIVMSGSVLCPWTQPPRNNWAYRLAQKLGYTGDNKDKAIF
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                                                                                                                                                                                                                                                  -NCESIKSLKFAPIENVTN-FKCLNIGDQFEVMALPELQKIEPVWNSFYAPNK
                                                                                                                                                                                                                                                                            NETEGMENVSWDPIKKSDEVYKCLNISDELKMIDVPEMDKIKQ-WESMFEKHR
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                                                                                                                                                                                                                                                                                                                                                                 KAYFGDEPCNQANMMKFLELCSYREFWHPIYRAALNRVRQSS-APTYLYRFDHDSK-LCN
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Pred. No. 1.4e-1
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Antiproliferative; cytostatic; cardiant; immunosuppressive; meiosis; antiinflammatory; antipsoriatic; dermatological; antifungal; mitosis antiparasitic; antimalarial; antirheumatic; antiarthritic; cell divicell cycle progression protein; tumour; proliferative disorder; cardiovascular; autoimmune; dermatological disorder.

mitosis;

division;

Drosophila

cell cycle progression

protein

#27.

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Query Match
Best Local S
Matches 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 8; Page 164; 213pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polynucleotides encoding cell cycle progression proteins, treating a tumor or a proliferative disorder -
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                         NHTSGTPVYLYRFDFDSEDLINPYRIMRSGRGVKGVSHADELTYFFWNQLAKRMPKESRE 493
                                                                                                                                                                                                      YQTADCVLPKHPREMVKTAWGNSIPTMMGNTSYEGLEFTSILKQMPMLVKELETCVNFVP
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RQSS-APTYLYRFDHDSK-LCNAIRIVLCGHQMRGVCHGDDLCYIFHSMLSHQSAPDSPE
                                                                                                                                  SELADAERTAPETLE-MGAKIKKAHVTGETPTADN---FMDLCSHIYFWFPMHRLLQLRF
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                    DKIKQ-WESMFEKHR
                                             HKVITGMVDVWTSFAAHGDP---NCESIKSLKFAPIENVTN-FKCLNIGDQFEVMALPEL 586
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3073
1 MNFNVSLMEKLKWKIKCIEN......PEMDKIKQWESMFEKHRDLF
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(:Species: Culex pipiens quinquefasciatus (southern house mosquito)
C:Date: 16:Nov-1990 #sequence_revision 13-Jan-1993 #text_change 21-Jul-2000
C:Accession: A35986
R:Mouches, C:: Pauplin, Y:: Agarwal, M:: Lemieux, L:: Herzog, M:: Abadon, M:: Beyssat
Proc. Natl. Acad. Sci. U.S.A. 87, 2574-2578, 1990
A:Title: Characterization of amplification core and esterase B1 gene responsible for A:Reference number: A35986; MUID:90207238; PMID:2320576
A:Accession: A35986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:M32328; NID:g156687; PIDN:AAA28289.1; PID:g156688 A;Note: the authors translated the codon CGT for residue 213 as Ala, and C;Superfamily: cholinesterase; cholinesterase homology
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A35986
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A;Molecule type: DNA
A;Residues: 1-540 <MOU>
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CGT

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## ALIGNMENTS

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Qy	Db	Qy	рь	Qy	Db	Qy	DЬ	Qy	Db	Qy	Db	Qy	Db	Qy	Ma	Qu
442 YLYRFDFDSEDLINPYRIMRSGRGVKGVSHADELTYFFWNQLAKRMPKESREYKTIERMT 501	355 ISMEKRIEFAAKLKORYYPDSIPSMENNLGYVHMMSDRVFWHGLHRTILARAAR-SRART 413	VTGET	298 IPKAPFEMARTAWGDKIDIMIGGTSEEGLLLLQKIKLHPELLSHPHLFLGNVPPNLK 354	325 LPKHPREMVKTAWGNSIPTMWGNTSYEGLFFTSILKOMPMLVKELETCVNFVPSELADAE 384	238 KAIGWDGQGGESGALRELRRAKPEDIVAHQEKLLTDQDMQDDIFTPFGPTVEPYLTEQCI 297	265 KLAGYKGEDNDKDVLEFLMKAKPQDLIKLEEKVLTLEERTNKVMFPFGGTVEPYQTADCV 324	178 FGGDPKRVTLAGHSAGAASVQYHLISDASKDLFQRRIVMSGSTYSSWSLTRQRNWVEKLA 237	205 FGGNPDNITVFGESAGAASTHYMMLTEQTRGLEHRGILMSGNAICPWANTQCQHRAFTLA 264	118 TELYGPDFLVQKDIVLVSFNYRIGALGFLCCQSEQDGVPGNAGLKDQNLAIRWVLENIAA 177	145 RDMYGPDYFIKKDVVLINIQYRLGALGFLSLNSEDLNVPGNAGLKDQVMALRWIKNNCAN 204	64 QCEPCYHFDRRLQKIVGCEDSLKINVFAKEINPSTPLPVMLYIYGGGFTEGTSG 117	VDFITG	4 ESLTVQTKYGPVRGKRNVSLLGQEYVSFQGIPYARAPEGELRFKAPVPPQKWTETLDCTQ 63	31 ETVVAETEYGKVKGVKRLTVYDDSYYSFEGIPYAQPPVGELRFKAPQRPTPWDGVRDC 88	; Indels 22; Gaps	Query Match 33.8%; Score 1038; DB 2; Length 540; Best Local Similarity 37 9%; Pred No 1 Ac-79.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----CNHKDKSVQVDEITGKVCGSEDCLYLSVYTNNLNPETKRPVLVYIHGGGFIIGENH 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RDMYGPDYFIKKDVVLINIQYRLGALGFLSLNSEDLNVPGNAGLKDQVMALRWIKNNCAN 204
                                                                                                                                                                                                                                                                                                                      LPKHPREMVKTAWGNSIPTMMGNTSYEGLFFTSILKQMPMLVKELETCVNFVPSELADAE
                                                                                                                                                                                                                                                                                                                                                                                                             KLAGYKGEDNDKDVLEFLMKAKPQDLIKLEEKVLTLEERTNKVMFPFGPTVEPYQTADCV 324
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                                                                                                                                                                                                                                                                                              IPKEPFEMARTAWGDKIDIMIGGTSEEGLLLLQKIKLQPELLSHPHLFLGNVPPNL---K
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                                                                                                                                                                      YLYRFDFDSEDLINPYRIMRSGRGVKGVSHADELTYFFWNOLAKRMPKESREYKTIERMT
                                                                                                                                                                                                                                                        RTAPETLEMGAKIKKAHVTGETPTADN---FMDLCSHIYFWFPMHRLLQLRFNHTSGTPV
                                                                                                                                                                                                                        ISMEKRIEFAAKLKORYYPDSSPSMENNLGYYHMMSDRVFWHGLHRTILARAAR-ŚRART
                                                                      GIWIQFATTGNPYSNEIEGMENVSWDPIKKSDEVYKCLNI-SDELKMIDVPEMDKIKQWE
                                                                                                                                              FVYRICLDSE-FYNHYRIMMIDPKLRGTAHADELSYLFSNFTQQVPGKETFEYRGLQTLV
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      carboxylesterase (EC 3.1.1.1) B - southern house mosquito (fragment) C;Species: Culex pipiens quinquefasciatus (southern house mosquito) C;Species: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 20-Sep-1999 C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 20-Sep-1999 C;Accession: S53372; S44212 R;Vaughan, A.; Rodriguez, M.; Hemingway, J. R;Vaughan, A.; Rodriguez, M.; Hemingway, J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem. J. 305, 651-658, 1995 Biochem
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RESULT 3
$53371
C;Accession: $5371
R;Yaughan, A.; Rederence unbern defence amplification of electrophoretically indisting A;Reference number: $53370
MUID:95134253; PMID:7530448
A;Reference number: $53370; MUID:95134253; PMID:7530448
A;Accession: $53370; MUID:95134253; PMID:7530448
A;Accession: $53370; MUID:95134253; PMID:7530448
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A; Molecule type: mRNA
A; Residues: 1-540 <VAU>
A; Cross-references: EMBL:Z32695; NID:9475069; PIDN:CAA83644.1;
A; Cross-references: strain MRES
A; Experimental source: strain MRES
C; Superfamily: cholinesterase; cholinesterase homology
C; Keywords: carboxylic ester hydrolase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPKHPREMVKTAWGNSIPTMMGNTSYEGLEFTSILKQMPMLVKELETCVNEVPSELADAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FGGNPDNITVFGESAGAASTHYMMLTEQTRGLFHRGILMSGNAICPWANTQCQHRAFTLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLAGYKGEDNDKDVLEFLMKAKPODLIKLEEKVLTLEERTNKVMFPFGPTVEPYOTADCV 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FGGDPKRVTLVGHSAGAASVQYHLISDASKDLFQRAIVMSGSTYNSWSLTRQRNWVEKLA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPKEPFEMARTAWGDKIDIMIGGTSEEGLLLLQKIKLQPELLSHPHLFLGNVPPNL---K
                                                                                                                                                                                                                                                                            ::|| ||| || || || || ::| ::| ||:| ||:: ::| ||:: ||:::| ||:::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||::::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||:::| ||
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                                                                                                                                                                                                                                                                                                                                                                                                                      ISMEKRIEFAAKLKORYYPDSSPSMENNLGYVHMMSDRVFWHGLHRTILARAAR-SRART 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RTAPETLEMGAKIKKAHVTGETPTADN---FMDLCSHIYFWFPMHRLLQLRFNHTSGTPV
                                                                                                                                      VDVFTAFVINGDP-NCSMTAKSGVVFEPNSQTKPTFKCLNIANDGLALVDYPDADRLDMW
                                                                                                                                                                                                  TGIWIOFATTGNPYSNEIEGMENVSWDPIKKSDEVYKCLNI-SDELKMIDVPEMDKIKOW
                                                                      ESMF 563
       534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.4%; Score 1025; DB 2;
37.3%; Pred. No. 1.4e-71;
tive 120; Mismatches 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
1.4e-71;
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indistinguishable

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A;Residues: 'SA',1-503 <VAN>
A;Cross-references: EMB1:Z33696; NID:g475070;
C:Superfamily: cholinesterase; cholinesterase
C:Keywords: carboxylic ester hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Experimental source: PelSS R;Vaughan, A.; Rodriguez, M.; Hemingway, J. submitted to the EMBL Data Library, April 1994 A;Description: The independent gene amplification A;Reference number: S44211 A;Accession: S44212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: S53
A; Accession: S53372
A; Molecule type: mRNA
A; Residues: 1-503 <VAU>
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-564 <HAN>
                                                                                                        R;Hanzlik, T.N.; Abdel-Aal, Y.A.I.; Harshman, L.G.; Hamm
J. Biol. Chem. 264, 12419-12425, 1989
A;Title: Isolation and sequencing of cDNA clones coding
                                                                                                                                                              juvenile-hormone esterase (EC 3.1.1.59) precursor - tobacco budworm
C;Species: Heliothis virescens (tobacco budworm)
C;Date: 22-Jun-1990 #sequence_revision 25-Sep-1992 #text_change 13-Sep-1998
C;Accession: A34325
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A; Residues: 'SA', 1-503 < VAW>
                                                     A; Reference number: A34325;
A; Accession: A34325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:Z32696
                                                                                          of the serine proteases
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LNPETKRPVLVYIHGGGFIIGENHRDMYGPDYFIKKDVVLINIQYRLGALGFLSLNSEDL 180
                                                                                                                                                                                                                                                                                                                                                     CLNI-SDELKMIDVPEMDKIKQWESMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DRVFWHGLHRTILARAAR-SRARTFVYRICLDSE-FYNHYRIMMIDPKLRGTAHADELFY 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GVPGNAGLQDQNLAIRWVLENIAAFGGDPKRVTLVGHSAGAASVQYHLISDASKDLFQRA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEGELRFKAPVPPQNWTETLDCTQQCEPCYHSDRRLQ-----KIVGCEDSLKINVFAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PVGELRFKAPQRPTPWDGVRDC-----CNHKDKSVQVDFITGKVCGSEDCLYLSVYTNN 120
                                                                                                                                                                                                                                                                                                                    CLNIANDGLAFVDYPDADRLDMWDAMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIYFWFPMHRLLQLRFNHTSGTPVYLYRFDFDSEDLINPYRIMRSGRGVKGVSHADELTY 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LQPELLSHPHLFLGNIPPNL---KISMEKRIEFAAKLKQRYYPDSSPSMANNLGYVHMMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QMPMLVKELETCVNFVPSELADAERTAPETLEMGAKIKKAHVTGETPTADN---FMDLCS 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ILMSGNAICPWANTQCQHRAFTLAKLAGYKGEDNDKDVLEFLMKAKPQDLIKLEEKVLTL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187;
                                                                                                                                                                                                                                                                                                                                                                                           LFSNFTQLVPDKKTFEYRGLQTLVDVFTAFVINGDP-NCSMTAKSGVVFEPNSQTKPTFK
                                                                                                                                                                                                                                                                                                                                                                                                                            FFWNQLAKRMPKESREYKTIERMTGIWIQFATTGNPYSNEIEGMENVSWDPIKKSDEVYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IVMSGSTYNSWSLTRQRNWVEKLAKAIGWDGQGGESGALRFLRAAKPEDIVANQEKLLTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30.2%;
36.9%;
                                                                         MUID:89308671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MUID:95134253;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 929; DB 2;
Pred. No. 3.6e-64;
D4; Mismatches 194
                                                                                                                                                                                                                                                                                                                    497
                                                                                                                                                                                                                                                                                                                                                         563
                                                                         PMID: 2745451
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                                                                                                           hormone
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                 Qy
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RESULT F89068 A;Cross-references: GB:J04955; NID:g159222; C;Superfamily: juvenile-hormone esterase C;Keywords: carboxylic ester hydrolase 밁 Ş В Qy В Qy В QΥ 밁 Qy 맑 Q DЬ Qγ В 20 밁 20 C;Date: 10-May-2001 #sequence\_revision
C;Accession: F89068 protein T28C12.4b [imported] - Caenorhabditis C; Species: Caenorhabditis elegans Matches 173; 487 132 482 426 254 194 192 136 428 369 369 309 310 252 77 83 18 Local YIHGGGFIIGENHRDMYGPDYFIKKDVVLINIQYRLGALGFLSLNSEDLNVPGNAGLKDQ DNILNATNEGPICFQTDVLYGRLMAASEMSEACIYANIHVPWQSL-PRVRGTTPLRPILV LAWQETNSRSVVAHLDSGIIRGVPR-SADGIKFASFLGVPYAKQPVGELRFKELEPLEPW M---PKESREYKTIERMTGIWIQFATTGNPYSNEIEGME 522 FTTSPLFAAYISKQLLQILGNQRDGSEEIHRQLIDLPAE---KLNEANAVLIEQIG--LT DGVRDCCNHKDKSVQVDFITGKVCG----SEDCLYLSVYT--NNLNPETK-----RPVLV 131 LHASPSEN-DVKMKNLMTGYFLNFIKCSQPTCEDNNSLE LAQKR-AETGGAPLYLYRFAYEGQNSIIK-KVM--GLNHEGVGHIEDLTYVFKVNSMSEA LLQLRFNHTSGTPVYLYRFDFDSEDLINPYRIMRSGRGVKGVSHADELTYFF-WNQLAKR QDNPTIIIPPKL~-LFMTPPELLMELAKTIERKYYNG-TISIDNFYKSCSDGFYEYPALK TFLPIVESPLPGVTTIIDDDPEILIAEGRGKNVPLLIGFTSSECETFRNRLLNFDLVKKI PFGPTVE-PYQTADCVLPKHPREMVKTAWGNSIPTMMGNTSYEGLFFTSILKQMPMLVKE ANTOCOHRAFTLAKLAGYKG--EDNDKDVLEFLMKAKPODLIKLEEKVLTLEERTNKVMF VTLLRWVQRNAKNFGGDPSDITTAGQSAGASAAHLLTLSKATEGLFKRAILMSGTGMSYF FIHGGGFAFGSGHEDLHGPEYLVTKNVIVITFNYRLNVFGFLSMNT--TKIPGNAGLRDQ LETCVNFVPSELADAERTAPETL-EMGAKIKKAHVTGETPTADNFMDLCSHIYFWFPMHR Similarity Conservative 22.5%; 102; Score 691; DB 2; Pred. No. 1.4e-45; 2; Mismatches 208 10-May-2001 PID:g159223 elegans #text\_change Length 564; Indels 36; 24-May-2001 Gaps 191 76 481 425 427 368 368 135 308 309 253 251 193 19;

F89068
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 24-May-2001
C;Accession: F89068
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Fittle: Genome sequence of the nematode C. elegans: a platform for investigating bio A;Fittle: Genome sequence of the nematode C. place of the nematode C. elegans: and www\_sanger.ac.uk/projects/C\_A;Mote: see websites genome.wustl.edu/gsc/C\_elegans/ and www\_sanger.ac.uk/projects/C\_A;Mote: see websites genome.wustl.edu/gsc/C\_elegans/ and www\_sanger.ac.uk/projects/C\_A;Mote: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Mote: see websites genome.wustl.edu/gsc/C\_elegans/ and www\_sanger.ac.uk/projects/C\_A;Mote: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Mote: see websites genome.wustl.edu/gsc/Celegans/ and www\_sanger.ac.uk/projects/C\_A;Mote: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Mote: see websites genome.wustl.edu/gsc/Celegans/ and www\_sanger.ac.uk/projects/C\_A;Mote: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Mote: see websites genome.wustl.edu/gsc/Celegans/ and www\_sanger.ac.uk/projects/C\_A;Mote: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Mote: see websites genome.wustl.edu/gsc/Celegans/ and www\_sanger.ac.uk/projects/C\_A;Mote: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Mote: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Mote: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Mote: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Mote: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Mote: published errata appeared in Scien

Matches

172;

Conservative

;86

Mismatches

220;

Indels 102;

Gaps

26;

22

FLNYRLTTNETVVAETEYGKVKGVKRLTVYDDSYYSFEGIPYAQPPVGELRFKAPQRPTP

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RESULT 7
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hypothetical protein T28C12.4a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T32053; T32054
C;Accession: T32053; T32054
R;Ledwith, J; Wohldmann, P.; Graves, T.; Bradshaw, H.
R;Ledwith, J; Wohldmann, P.; Graves, T.; Bradshaw, H.
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R;Ledwith J; Wohldmann, P.; Gra
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A;Experimental source: strain Bristol N2; clone T28C12
A;Accession: T32054
                                                                                                                                                                                                                    A; Experimental source: strain Bristol to C; Genetics: A; Gene: CESP: T28C12.4a; CESP: T28C12.4b A; Map position: 5
A; Introns: 70/1; 96/3; 137/3; 192/3; 36 C; Superfamily: cholinesterase; cholines
                                                                                                                                                                                                                                                                                                                                                                 A;Status: Professor type: DNA
A;Molecule type: DNA
A;Residues: 81-658 <LE2>
A;Cross-references: EMBL:AF016679; PIDN:AAB66160.1; GSPDB:GN00023; CESP:T28C12.4b
A;Cross-references: EMBL:AF016679; PIDN:AAB66160.1; GSPDB:GN00023; CESP:T28C12.4b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-658 <LED>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAI-----GLLRGTEKEINSAIDVLSRKNRLSRSKIE--AMTEK--VYGDSPALRADSKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSILKOMPMLVKELETCVNFVPSELADAERTAPETLEMGAKIKKAHVTGETPT--ADN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TMFFSNTIFKECQLPLAPVIDGE-----ILPHDLKVLRETQ--EHVPSLVGGGEYEALLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----TGGTHTSELSYLFDCNYMSAPLGMNKTD-KVVSGMTADYFTNFVKFGTPNGPNS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RKMETVQLISDIFANYGNYRF--MRDCQQRGVECYGYSFDHQSKQMWGWLQHVVPF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----FMDLCSHIYFWFPMHRLLQLRFNHTSGTPVYLYRFDFDSEDL-----INPYRIMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EIEGMENVSWDPIKKSDEVYKCLNISDELKMIDVPEMDKIKQWESM--FEKH
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-QLPKWERISPDDEHMKLISIKPE-----PEMKTTVYGYRMQNFEDH
                                                                                                                                                                                                                              cholinesterase; cholinesterase homology
                                                                                                 19.3%;
milarity 29.1%;
Conservative 98
                                                                                                                                                                                                                                                            96/3; 137/3; 192/3; 366/2; 423/1; 480/3; 573/2
                                                                                                               98;
                                                                                                        Score 593; DB 2; I
Pred. No. 7.1e-38;
8; Mismatches 220;
                                                                                                                                                                           Length 658;
                                                                                                                     Indels 102;
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A;Residues: 1-547 <JON>
C;Superfamily: juvenile-hormone esterase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;IILLE: Structure, expression and gene sequence of a juvenile hormone esterase-relat A;Reference number: S55233; MUID:95031924; PMID:7945209
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FIIGENHRDMYGPDY------FIKKDVVLINIQYRLGALGFLSLNSEDLNVPGNAGLK 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WEGIRKCNKYPNRSIHKEMPWDKALPSANQSEDCLYLNVFAPKIREDKKYPVLFYIHGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAI-----GLLRGTEKEINSAIDVLSRKNRLSRSKIE--AMTEK--VYGDSPALRADSKA 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KVLTLEERTNKVMFPFGPTVEPYQTADCVLPKHPREMVKTAWGNSIPTMMGNTSYEGLFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----FMDLCSHIYFWFPMHRLLQLRFNHTSGTPVYLYRFDFDSEDL-----INPYRIMR 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TSILKQMPMLVKELETCVNFVPSELADAERTAPETLEMGAKIKKAHVTGETPT--ADN--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----QLPKWERISPDDEHMKLISIKPE----PEMKTTVYGYRMQNFEDH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGRGVKGVSHADELTYFF-WNQLAKRMPKESREYKTIERWTGIW----IQFATTGNPYSN
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                                                                                                                                                                                                                                                                                                                                                                                                VNCMLWPNIDQRYHANQRPQCDVRAQLDSGWVCGSIRSAEEGVQYASFRGIPYAQQPLGQ 77
                                                                                                                                                                                                                                                                                                            LREKAPORPTPWDGVRDCCNHKDKSVQVDFITGKV-----CGSEDCLYLSV-----YTNN 120
                                               NQTANYLPILVFIHGGGFQIGSSGSDIHGPEYLMSKGVIVITFNHRLNVFGYLSLNS--T
                                                                                                                                                                                                   LNPETKRPVLYYIHGGGFIIGENHRDMYGPDYFIKKDVVLINIQYRLGALGELSLNSEDL 180
                                                                                                                                                                                                                                                                LREKELOPLKPWNGVLETIEEGPICPQYDEIYGRMGQPTAMSEACIYANVHVPFNEYTSY 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.1%; Score 585.5; DE 29.7%; Pred. No. 2e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
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RESULT 9
B69680

para-nitrobenzyl esterase (EC 3.1.1.-) - Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bocollus subtilis
C;Species: Bacillus subtilis
C;Species: Bocollus subtilis
C;Species: Bacillus subtilis
Bacillus subtilis
A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                      A;Cross-references: EMBL:U06089; NID:9468045; PIDN:AAAI A;Experimental source: strain NRRL B8079 C;Genetics: A;Gene: pnbA C;Superfamily: cholinesterase; cholinesterase homology C;Keywords: carboxylic ester hydrolase F;24-478/Domain: cholinesterase homology <CHE>
                       Ş
                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-58,'P',60-94,'Q',96-149,'D',151-229,'A',231-241,'S',243-245,'R',247-250,'A;Cross-references: EMBL:U06089; NID:9468045; PIDN:AAA81915.1; PID:9468046
A:Experimental source: strain NRRL B8079
                                                                                                                                                                                                                                                                                                                                                                  Gene 151, 37-43, 1994
A; Title: The Bacillus subtilis pnbA gene encoding p-nitrobenzyl A; Reference number: 140510; MUID:95129891; PMID:7828905
                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:Z99121; GB:AL009126; NID:g2635827; PIDN: A;Experimental source: strain 168
R;Zock, J.; Cantwell, C.; Swartling, J.; Hodges, R.; Pohl, T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
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                                                                                                                                                                                                                                                                                                                             A; Status: preliminary; translated from GB/EMBL/DDB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                  A; Accession: I40510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-489 < KUN>
                                                                   Matches
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SHIYFWFPMHRLLQLRFNHTSGTPVYLYRFDFDSEDLINPYRIMRSGRGVKGVSHADELT:::| :| :| :| :| :| :::|
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IIYLDLIGLIKENPSVA--LPVNMSYSV-SAKKSFDLYQMISDRYFQGNL-TVENYLPYC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ILMSGVATAGFYTTSPSYTQMVAQMFLGNVGINSTDADEIHDQLVQMP---LEKIMEANRI
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                                                                   162;
                                                                                      Similarity
                                                                 Conservative
                                                                               18.8%;
29.2%;
                                                                 89;
                                                            Score 578.5; DB 2;
Pred. No. 6.1e-37;
9; Mismatches 191;
                                                              Indels
                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIDN:CAB15444.1; PID:g2635952
                                                                                                      489;
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                                                          Qγ
                                                                                                    DЬ
                                                                                                                                                                                                                                                                C;Genetics:
A;Gene: CESP:F15A8.6
A;Map position: X
A;Introns: 23/3; 165/2; 247/1;
C;Superfamily: cholinesterase;
                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, April 1997
A;Description: The sequence of C. elegans cosmid
A;Reference number: Z20069
A;Accession: T25690
A;Status: preliminary; translated from GB/EMBL/DD
A;Residues: 1-583 <MIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
T25690
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                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:U97549; PIDN:AAB52848.1; GSPDB:GN00028; CESP:F15A8 A;Experimental source: strain Bristol N2; clone F15A8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Miller,
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                                                                                                                                          LTTNETVVAETEYGKVKGVKRLTVYDDSYYS-FEGIPYAQPPVGELRFKAPQRPTPWDGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VPSELADAERTAPETLEMGAKIKKAHVTGETPTADNFMDL------CSHIYFWFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WVRENISAFGGDPDNVTVFGESAGGMSIAALLAMPAAKGLFQKAIMESGASRTMTKEQAA
                       KKCVRFGPRAPQADFFWERFTLGVGKSEDCLYLNVFSPTWKAEEVSNGVGFFKPICGKIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LDSEITIENDPESEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVAYASAQSHY---APVWMYRFDWHPKK--PPY-----NKAFHALELPFVFGNLDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MHRLLQLRENHTSGTPVYLYREDEDSEDLINPYRIMRSGRGVKGVSHADELTYFFWN-QL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PK----TLPEEPEKAIAEGAASGIPLLIGTTRDEGYLFFT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STSAAFLQVLGINEGQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WIKNNCANFGGNPDNITVFGESAGAASTHYMMLTEQTRGLFHRGILMSGNAICPWANTQC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----PDSDVHSQETLDAALE----YLLGK-PLAEKVADLYPRSLESQIHMMTDLLFWRP
                                                                                                                                                                                    Conservative
                                                                                                    -RTRNGLVEGF-RIKIDDDREVDMFLGIPFAKAPVGDLRFKNPEHTEDWDGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -GSICPQPSDLLSLSYTELPRQSEDCLYVNVFAPD-TPSKNLPVMVWIHGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #sequence_revision 15-Oct-1999 #text_change
                                                                                                                                                                                                                                                                247/1; 294/1; 432/3; 481/1; 524/2 terase; cholinesterase homology
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                                                                                                                                                                                    97;
                                                                                                                                                                                Score 571.5; DB 2
Pred. No. 2.8e-36;
7; Mismatches 229
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464

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Carboxylesterase (EC 3.1.1.) FE4 precursor - green peach aphid C;Species: Myzus persicae (green peach aphid)
C;Dete: 10-Sep-1999 *sequence_revision 10-Sep-1999 *text_change 10:Sep-1999
C;Accession: $36787
C;Accession: $36787
R;Field, L.M.; Williamson, M.S.; Moores, G.D.; Devonshire, A.L.
Blochem. J. 294, 569-574, 1993
A;Title: Cloning and analysis of the esterase genes conferring insecticide res. A;Title: Cloning and analysis of the esterase genes conferring insecticide res. A;Reference number: $36786; MUID:93384534; PMID:8373371
A;Reference number: $36786; MUID:93384534; PMID:8373371
A;Accession: $36787
A;Accession: $36786
A;Accession: $36786
A;Accession: $36787
A;Accession: $36786
A;Accession: $36787
A;Cross-references: EMBL:X74555; NID:9397512; PIDN:CAA52649.1; PID:9397513
A;Cross-references: EMBL:X74555; NID:9397512; PIDN:CAA52649.1; PID:9397513
C;Superfamily: Cholinesterase; Cholinesterase homology
C;Keywords: carboxylic ester hydrolase
C;Keywords: carboxylic ester hydrolase
C;Keywords: carboxylic ester hydrolase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DQVCPGNLGLWDMTMALQWVRDNVHAFGGDPRKVTVFGQSAGGVSVDLLSLSPHSRDLFH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCEHEGLLFASLGPSNFDEKGIDKLLALLITE-----ENHEDFEALREEAKKMYLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NTSYEGLEFTS-----ILKQMPMLVKELETCVNFVPSELADAERTAPETLEMGAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RE---FEKRLLTRKGVDVSKIGLDLAPVIGS-KPSD-FLPKSIEELRKEAPKKNÍ--MVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YGNPNGQYEDSTVFDFKWEPTSK-EEPTNFLAINEKKCEMQTVYQDNRAEFWKKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -- CNPRSFGILSLRAPFRAATHCTELAYIFGVSIVFNYRYNESDRAMLDLMTKMWTNFAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGNPYSN-EIEGMENVSWDPIKKSDEVYKCLNISD-ELKMIDVPEMDKIKQWESM
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                                                                                                                                                                                                                                                                                                           TTNETYVAETEYGKVKGVKRLTVYDDSYYSFEGIPYAQPPVGELRFKAPQRPTPWDGVRD
                                                                                                                                                                                                                                  CCNHKDKSVQVDFITG-KVCGSEDCLYLSVYTNNLNPETK----RPVLVYIHGGGFIIGE
                                                                                                                                                                                                                                                                    SASNTPKVQVHSGEIAGGFEYTYNGRKIYSFLGIPYASPPVQNNRFKEPQPVQPWLGVWN
                                                                           CANFGGNPDNITVFGESAGAASTHYMMLTEQTRGLFHRGILMSGNAICPWANTQ-CQHRA
                                                                                                                  G--ILYGPHYLLDNNDFVYVSINYRLGVLGFAS--TGDGVLPGNNGLKDQVAALKWIQQN
                                                                                                                                                  NHRDMYGPDYFI-KKDVVLINIQYRLGALGFLSLNSEDLNVPGNAGLKDQVMALRWIKNN
                                                                                                                                                                                           ATVPGSACLGIEFGSGSKIIGQEDCLFLNVYTPKLPQENSAGDLMNVIVHIHGGGYYFGE
  FTLAKLAGYKGEDNDKDVLEFLMKAKPQDLIKLEEKVLTLEERTNKVMFPFGPTVE--PY
                                      IVAFGGDPNSVTITGMSAGASSVHNHLISPMSKGLFNRAIIQSGSAFCHWSTAENVAQKT
                                                                                                                                                                                                                                                                                                                                                                    18.5%;
                                                                                                                                                                                                                                                                                                                                                  Score 568.5; DB 1;
Pred. No. 4.5e-36;
8; Mismatches 217;
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                                                                                                                                                                                                                                                                                                                                                                                             Length
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C;Species: Homo Sapiens (man)
C;Date: 30 - Jun-1987 #sequence_revision 23-Feb-1996 #text_change 08-Dec-2000
C;Accession: A33769; A26613; A33887; A34668; A00772
C;Accession: A33769; A26613; A33887; A34668; A00772
R;Arpagaus, M; Kott, M,; Vatsis, K.P.; Bartels, C.F.; La Du, B.N.; Lockrid; Biochemistry 29, 124-131, 1990
A;Title: Structure of the gene for human butyrylcholinesterase. Evidence for A;Reference number: A33769; MUID:90212557; PMID:2322535
A;Accession: A33769
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ACHU

cholinesterase (EC 3.1.1.8) precursor [validated] - human

cholinesterase; choline acylhydrolase; butyrylcholinesterase; choline esterase

N;Alternate names: acylcholine acylhydrolase; butyrylcholinesterase; choline esterase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 'MSVQSNLQAGAAAASCISPKYYMIFTPCKLCHLCCRESEIN', 1-602 <ARP>
A; Cross-references: GB:M32391; GB:J02879
A; Cross-references: GB:M32391; GB:J02879
A; Note: two ATG codons found upstream of Met-1 do not lie in a favorable c
A; Note: two ATG codons found upstream of Met-1 do not lie in a favorable c
A; Prody, C.A.; Zevin-Sonkin, D.; Gnatt, A; Goldberg, O.; Soreq, H.
Proc. Natl. Acad. Sci. U:S.A. 84, 355-3559, 1987
Proc. Natl. Acad. Sci. U:S.A. 84, 355-3559, 1987
A; Title: Isolation and characterization of full-length cDNA clones coding
A; Reference number: A26613; MUID:87231856; PMID:3035536
A; Accession: A26613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 'MSVQSNLQAGAAAASCISPKYYMIFTPCKLYHLCCRESEIN', 1-602 <MCT>
A; Residues: 'MSVQSNLQAGAAAASCISPKYYMIFTPCKLYHLCCRESEIN', 1-602 <MCT>
A; Note: two ATG codons found upstream of Met-1 do not lie in a favorable context
A; Nogueira, C.P.; McGuire, M.C.; Graeser, C.; Bartels, C.F.; Arpagaus, M.; Van de
R; Nogueira, C.P.; McGuire, M.C.; Graeser, C.; Bartels, C.F.; Arpagaus, M.; Van de
Am. J. Hum. Genet. 46, 934-942, 1990
A, Title: Identification of a frameshift mutation responsible for the silent pheno
A; Title: Identification of a frameshift mutation responsible for the silent pheno
A; Reference number: A34668; MUID:90252779; PMID:2339692
A; Recession: A34668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-133,'D',135-602 <PRO>
A; Residues: 1-133,'D',135-602 <PRO>
R; McTiernan, C.; Adkins, S.; Chatconnet, A.; Vaughan, T.;
Proc. Natl. Acad. Sci. U.S.A. 84, 6682-6686, 1987
Proc. Natl. Acad. Sci. U.S.A. 84, 6682-6686, 1987
A; Title: Brain cDNA clone for human cholinesterase.
A; Reference number: A33887; MUID:88016155; PMID:3477799
A; Accession: A33887
                                                                                          A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 143-145, VSNWNIFTCL' <NOG>
A; Residues: 143-145, USNWNIFTCL' <NOGO
A; Note: frameshift mutant in codon for residue 145 (Gly)
A; Note: frameshift mutant in codon for residue 145 (Gly)
A; Lockridge, O.; Bartels, C.F.; Vaughan, T.A.; Wong, C.K.; Norton, S
B; Lockridge, O.; Bartels, C.F.; Vaughan, T.A.; Wong, C.K.; Norton, S
B; Lockridge, O.; Bartels, C.F.; Vaughan, T.A.; Wong, C.K.; Norton, S
B; Lockridge, O.; Bartels, C.F.; Vaughan, T.A.; Wong, C.K.; Norton, S
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B; Lockridge, O.; Bartels, C.F.; Vaughan, T.A.; Wong, C.K.; Norton, S
B; Lockridge, O.; Bartels, C.F.; Vaughan, T.A.; Wong, C.K.; Norton, S
B; Lockridge, O.; Bartels, C.F.; Vaughan, T.A.; Wong, C.K.; Norton, S
B; Lockridge, O.; Bartels, C.F.; Vaughan, T.A.; Wong, C.K.; Norton, S
B; Lockridge, O.; Bartels, C.F.; Vaughan, T.A.; Wong, C.F.; Norton, S
B; Lockridge, O.; Bartels, C.F.; Vaughan, T.A.; Wong, C.F.; Vaughan, C.F.; Vaughan, S
B; Lockridge, O.; Bartels, C.F.; Vaughan, T.A.; Wong, C.F.; Vaughan, S
B; Lockridge, O.; Bartels, C.F.; Vaughan, T.A.; Wong, C.F.; Vaughan, S
B; Lockridge, O.; Bartels, C.F.; Vaughan, C.F.; Vau
Experimental source: plasma Comment: Cholinesterase is
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                                   (except erythrocytes).
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A;Gene: GDB:BCHE; CHEI
A;Cross-references: GDB:120558; OMIM:177400
A;Map position: 3q26.13q26.2
A;Introns: 506/2; 562/1
C;Function:
A;Description: hydrolyzes acylcholines to choline and a carboxylic acid
A;Note: this cholinesterase is highly reactive with organophosphate ester
C;Superfamily: cholinesterase; cholinesterase homology
C;Keywords: carboxylic ester hydrolase; glycoprotein; homotetramer
F;1-28P,Domain: signal sequence #status predicted <SIC>
F;29-602/Product: cholinesterase homology <CHE>
F;45,85,134,269,284,39,483,509,514,7Binding site: carbohydrate (Asn) (cov
RESULT 13

S36786

S36786

Carboxylesterase (EC 3.1.1.1) E4 - green peach aphid
C.Species: Myzus persicae (green peach aphid)
C;Date: 09-Jun-1994 #sequence_revision 01-Dec-1995 #text_change
C;Accession: S36786
R;Field, L.M.; Williamson, M.S.; Moores, G.D.; Devonshire, A.L.
Biochem. J. 294, 569-574, 1993
A;Title: Cloning and analysis of the esterase genes conferring i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QYRLGALGFLSL--NSEDLNVPGNAGLKDQVMALRWIKNNCANFGGNPDNITVFGESAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---SEDCLYLNVWIPAPKPK-NATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VCGSEDCLYLSVYTNULNPETKRPVLVYIHGGGFIIGENHRDMYGPDYFIKKD-VVLINI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KVTIICI--RFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGM-NLTVFGGTVTAFLGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KWKIKCIENKFLNYRLT-----TNETVVAETEYGKVKGVKRLTVYDDSYYSFEGIP
                                                                                                                                                                                                                                   WESMFEK
                                                                                                                                                                                                                                                                       SIVKRWANFAKYGNP--NETQN-NSTSWPVFKSTEQKYLTLN-TESTRIMTKLRAQQCRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KKTQILVGVNKDEGTAF -- LVYGAPGFSKDNNSII -- TRKEFQEGLKIFFPGVSEFGKES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NSIPTMMGNTSYEGLFFTSILKQMPMLVKELETCVNFVPSELADAERT-APETLEMGAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASTHYMMLTEQTRGLFHRGILMSGNAICPWANT---QCQHRAFTLAKLAGYKGEDNDKDV 278
                                                                                                                                                                                                                                                                                                     RMTGIWIQFATTGNPYSNEIEGMENVSWDPIKKSDEVYKCLNISDELKMIDVPEMDKIKQ
                                                                                                                                                                                                                                                                                                                                                                           TPYYLYRFDFDSEDLINPYRIMRSGRGVKGVSHADELTYFFWNQLAKRMPKESREYKTIE 498
                                                                                                                                                                                                                                                                                                                                                                                                                ILFHYTDWVDDQRPENYREALGDVVGDYNFICPALEFTKKFSEW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IKCLRNKDPQEILLNEAFVVPY---GTPLSVNFGPTVDGDFLTDM-----PDILLELGQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASVSLHLLSPGSHSLFTRAILQSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRE-NETEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                    565
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29.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 568.5; DE Pred. No. 5e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                          GVMHGYEIEFVFGLPLERRDNYTKAEEILSR
                                                                                                                                                                                                                                                                                                                                                                                                                                               -LCSHIYF-----WFPMHRLLQLRENHTSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
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   insecticide
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   resistance
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A;Reference number: S36786
A;Accession: S36786
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-552 <FIE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        FTLAKLAGYKGEDNDKDVLEFLMKAKPQDLIKLEEKVLTLEERTNKVMFPFGPTVE--PY
                                                                                                                                                                                                                                                                                                                                                                                                                                         G--ILYGPHYLLDNNDFVYVSINYRLGVLGFAS--TGDGVLTGNNGLKDQVAALKWIQQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCNHKDKSVQVDFITG-KVCGSEDCLYLSVYTNNLNPETK----RPVLVYIHGGGFIIGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTNETVVAETEYGKVKGVKRLTVYDDSYYSFEGIPYAQPPVGELRFKAPQRPTPWDGVRD
                             SDEVYKCLNISDELKMIDVPEMDKIKQWE
                                                            VLKMDGFY---
                                                                                                                        FGYGTSKAAQ-
                                                                                                                                                     FWFPMHRLLQLRFNHTSG----TPVYLYRFDFDSEDLINPYRIMRSGRGVKGVSHADELTY
                                                                                                                                                                                      ILD----YNYTISNENLRFKTAQDI---
                                                                                                                                                                                                                   LVKELETCVNFVPSELADAERTAPETLEMGAKIKKAHVTGETP----TADNFMDLCSHIY
                                                                                                                                                                                                                                                  EK---FLPDIPEKLVP----HDIPVLISIAQDEGLIFSTFLGLENGFNELNNWNEHLPH
                                                                                                                                                                                                                                                                                 KYIANLMGCP-TNNSVEIVECL-RSRPAKAI--AKSYLNEMPWRNEPETPEGPTVEVAGY
                                                                                                                                                                                                                                                                                                                                                                            IVAFGGDPNSVTITGMSAGASSVHNHLISPMSKGLFNRAIIQSGSAFCHWSTAENVAQKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATVPGSACLGIEFGSGSKIIGQEDCLFLNVYTPKLPQENSAGDLMNVIVHIHGGGYYFGE
                                                                                 -FFWNQLAKRMPKESREYKTIERMTGIWIQFATTGNPYSNEIEGMENVSWDPIKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.5%;
nilarity 29.3%;
Conservative 8
NLADPFRETKITQQQTFEARE
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                                                                                                                        ----HIAAKNTAPVYFYEFGYSGNYSYVAFFDPKSYSRGSSPTHGDETSY
                                                            -VYDNEEDRKMIKTMVNIWATFIKSGVPDTENSE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 567; DB 2;
Pred. No. 5.7e-36;
B; Mismatches 226
                             560
538
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                                                                                                                                                                                    KEFYFGDKPISKETKSNLSKMISDRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIDN:CAA52648.1; PID:g397511
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acetylcholinesterase (EC 3.1.1.7) precursor, 11s form [validated] - Pacific N;Alternate names: acetylcholinesterase, asymmetric form C:Species: Torpedo californica (Pacific electric ray) C;Date: 17-Mar-1987 #sequence\_revision 08-Nov-1996 #text\_change 15-Sep-2000 C;Accession: A00773; A60820; A31962; B31962; A23902; B41117; S15677 A; Molecule type: mRNA A; Residues: 'NS',11-596 <SCH> A; Cross-references: GB:X03439; NID:g64389 A; Experimental source: electric organ A; Note: parts of this sequence, including R; Schumacher, M.; Camp, S.; Maulet, Y.; N Nature 319, 407-409, 1986
A; Title: Primary structure of Torpedo californica
A; Reference number: A00773; MUID:86118676; PMID:37
A; Accession: A00773 R;Schumacher, 407-409, 1986 s.; Maulet, Y.; Newton, rornica acetylcholinesterase
pMID:3753747 **.** MacPhee-Quigley, Pacific K.; Taylor, deduced electric from

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Taylor, S.

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carboxyl ends

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A; Residues: 499-555 <SCA'>
A; Residues: 499-555 <SCA'>
A; Cross references: GB:NO3/39; NID:964389
A; Cross references: GB:NO3/39; NID:964089
A; Cross references: GB:NO3/39; NID:96408285; PMID:3900071
A; Macchee-Quisley, K.: Taylor, P.: Taylor, S.
Biol. Chem. 260, 12185-12189, 1985
J. Biol. Chem. 260, 12185-12189, 1985
J. Biol. Chem. 260, 12185-12189, 1985
J. Biol. Chem. 260, 12185-12189, 1985
J. Biol. Chem. 260, 12185-12189, 1985
J. Biol. Chem. 260, 12185-12189, 1985
J. Biol. Chem. 260, 12185-12189, 1985
J. Biol. Chem. 260, 12185-12189, 1986
J. Reference number: A23902; MUID:86008285; PMID:3900071
A; Mccession: Biol. Chem. 261, 1356-13570
A; Mccession: B4117
A; Mccession: B4117; MUID:91296772; PMID:2068091
A; Mccession: B4117; MUID:91296772; PMID:2068091
A; Mccession: B4117; MUID:91296772; PMID:2068091
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A; Mccession: B4117; MUID:91296772; PMID:2068091
A; Mccession: B4117; MUID:91296772; PMID:206806
A; Mccession: B4187; Mcce
R; Sussman, J.L.; Harel, M.; Frolow, F.; Oeffrer, C.; Goldman, A.; Toker, L.; Silman, I. Science 253, 872-879, 1991

A; Title: Atomic structure of acetylcholinesterase from Torpedo californica: a prototypic A; Teference number: A43098; MUID:91343928; PMID:1678899

A; Reference number: A43098; MUID:91343928; PMID:1678899

A; Comment: Synapses usually contain this 11s (asymmetric) form of cholinesterase with a C; Comment: Synapses usually contain this 11s (asymmetric) form of cholinesterase with a C; Comment: 11s form is disulfide linked homodimer; 18s form is homotetramer, a dimer of C; Complex: 11s form is disulfide linked homodimer; 18s form is homotetramer, a dimer of C; Complex: 11s form is disulfide linked homodimer; 18s form is homotetramer, a dimer of C; Enction: hydrolyzes acetylcholine to choline and acetate

A; Description: hydrolyzes acetylcholine to choline and acetate

A; Pathway: neurotransmitter degradation
C; Superfamily: cholinesterase; cholinesterase homology
C; Keywords: alternative splicing; carboxylic ester hydrolase; glycoprotein; membrane professory acetylcholinesterase, 11s form #status experimental <MAT>
F; 22-596/product: acetylcholinesterase, 11s form #status experimental <MAT>
F; 80,478,554/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Primary structure of acetylcholinesterase: implications for regulation A;Title: Primary structure of acetylcholinesterase: implications for regulation A;Reference number: A60820; MUID:87054662; PMID:3536598
A;Reference number: A60820; MUID:87054662; PMID:3536598
A;Reference number: A60820; MUID:87054662; PMID:3536598
A;Reference number: A92701; MUID:89066695; PMID:3198606
A;Reference number: A92701; MUID:89066695; PMID:3198606
A;Reference number: A92701; MUID:89066695; PMID:3198606
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A; Residues: 1-23 <SC32
A; Cross-references: EMBL: X03439; NID: 964389
A; Cross-references: EMBL: X03439; NID: 964389
A; Experimental source: clones AChE-11 and AChE-18
A; Note: revision to sequence A00773
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A; Residues: 499-565 <SC4>
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F:105/Binding site: substrate (Trp) #status experimental F:221/Active site: Ser #status experimental F:221/Active site: Glu, His #status predicted F:348,461/Active site: Glu, His #status predicted F:347/Binding site: Carbohydrate (Asn) (covalent) #status F:593/Disulfide bonds: interchain #status experimental
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                                                                                                                                                                                                                                        acetylcholinesterase (EC 3.1.1.7) precursor - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Dete: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 18-Jun-1999 C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 18-Jun-1999 C;Accession: JH0314
C;Accession: JH0314
R;Rachinsky: T.L.; Camp, S.; Li, Y.; Ekstroem, T.J.; Newton, M.; Taylor, P.
Neuron 5, 317-337, 1990
A;Title: Molecular cloning of mouse acetylcholinesterase: tissue distributic A;Reference number: JH0314; MUID:90380429; PMID:2400605
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A;Cross-references: EMMBL:x56518; NID:g49844; PIDN:CAA39867.1; | A;Cross-references: EMMBL:x56518; NID:g49844; PIDN:CAA39867.1; | A;Experimental source: brain
C;Superfamily: cholinesterase; cholinesterase homology
C;Superfamily: cholinesterase; glycoprotein; membrane
C;Keywords: carboxylic ester hydrolase; glycoprotein; membrane
C;Keywords: carboxylic ester hydrolase; predicted <SIG>F;1-31/Domain: signal sequence #status predicted <MAT>F;32-614/Product: acetylcholinesterase #status predicted
F;33-69/Domain: cholinesterase homology <CHE>F;63-569/Domain: cholinesterase homology <CHE>F;100-127,288-303,440-560/Disulfide bonds: #status predicted
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A; Residues: 1-614 <RAC>
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15-JUL-1998 (Rel. 36, Last annotation update)
15-JUL-1998 (Rel. 36, Last annotation update)
15-JUL-1998 (Rel. 36, Last annotation update)
Juvenile hormone esterase precursor (EC 3.1.1.59) (JH
Heliothis virescens (Noctuid moth) (Owlet moth)
Heliothis virescens (Noctuid moth), Annotabulate; Pancrusta
Eukaryota; Metazoa; Arthropoda; Mandibulate; Pancrusta
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SEQUENCE FROM N.A., AND SEQUENCE OF 20-54.

MEDLINE-89308671; PubMed-2745451;

Hanzlik T.N., Yehia A.I.A.-A., Harshman L.G., Hammock B.D.;

Hanzlik T.N., Yehia A.I.A.-A., Harshman L.G., Hammock B.D.;

"Isolation and sequencing of cDNA clones coding for juvenile hormone
"Isolation and sequencing of cDNA clones coding for juvenile hormone
esterase from Heliothis vicescens. Evidence for a catalytic mechanism
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PIR; A34325; A34325
HSSP; P37967; 1QE3
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VARIANT
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                                                                                                                                                                  VTLLRWVQRNAKNFGGDPSDITIAGQSAGASAAHLLTLSKATEGLFKRAILMSGTGMSYF
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AQKR-AETGGAPLYLYRFAYEGQNSIIK-KVM--GLNHEGVGHIEDLTYVFKVNSMSEAL
                                         FLPIVESPLPGVTTIIDDDPEILIAEGRGKNVPLLIGFTSSECETFRNRLLNFDLVKKIQ
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                      LQLRENHTSGTPVYLYRFDFDSEDLINPYRIMRSGRGVKGVSHADELTYFF-WNQLAKRM
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2; Mismatches 209
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Electrophoridae; Electrophorus.
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                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar entities requires a license agreement (See http://www.isb-
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Acetylcholinesterase precursor (EC 3.1.1.7) (AChE).
                                                                                                                                                                                                                                                                                                         InterPro; IPR002018; CarbesteraseB.
InterPro; IPR000997; Cholinesterase.
InterPro; IPR000379; Ser_estrs_site.
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PRINTS; PR00878; CHCLNESTRASE.
PROSITE; PS00122; CARBOXYLESTE
PROSITE; PS00941; CARBOXYLESTE
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                                                                                                                                                                                                                               Neurotransmitter
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BIOL Chem. 272:33045-33055(1997).

FUNCTION: RAPIDLY HYDROLYZES CHOLLINE RELEASED INTO THE SYNAPSE. CATALYTIC ACTIVITY: Acetylcholline + H(2)0 - cholline + acetate. SUBUNIT: DIMERS AND COLLAGEN-TAILED FORMS, IN WHICH CATALYTIC TETRAMERS ARE ASSOCIATED WITH ANCHORING PROTEINS THAT ATTACH THEM TO THE BASAL LAMINA OR TO CELL MEMBRANES, IN THE COLLAGEN-TAILED FORMS, SUBUNITS ARE ASSOCIATED WITH A SPECIFIC COLLAGEN, COLO, WHICH TRIGGERS THE FORMATION OF ISOFORM T TETRAMERS FROM DIMERS. MISCELLAMEOUS: NO OTHER ISOFORM SESTET. THIS PROTEIN CORRESPONDS TO THE TISOFORM IN OTHER SPECIES.

MISCELLAMEOUS: NO OTHER SPECIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collab
een the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
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Best Local :
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                                                                                                                                                                           01-0CT-1994
01-0CT-1994
16-0CT-2001
                                                                                                                                                                                                           PNBA_BACSU
P37967;
                   cloning, sequence and Gene 151:37-43(1994).
                           Rosteck P. Jr., McGilvray D., Que
"The Bacillus subtilis pnbA gene
cloning, sequence and high-level
                                                                                     STRAIN=NRRL
                                                              MEDLINE=95129891;
Zock J., Cantwell
                                                                                               SEQUENCE
                                                                                                                                  Bacteria;
                                                                                                                                           Bacillus
                                                                                                                                                       PNBA
                                                                                                                                                                  Para-nitrobenzyl
                                                                                                                     NCBI_TaxID=1423;
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                                                                                                                                                                                                                                                                              ENIDDAERQWKAEFHR
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                                                                                                                                                                                                                                                                                                EM--DKIKQWESMFEK
                                                                                                                                                                                                                                                                                                                       PNIN-VDGSIDSRRRWPVFTSTEQKHVGLN-TDSLKVHKGLKSQFCALWNRFLPRLLNVT
                                                                                                                                                                                                                                                                                                                                            PYSNEIEGM -- ENVSWDPIKKSDEVYKCLNISDELK --
                                                                                                                                                                                                                                                                                                                                                                   LVWPEWM
                                                                                                                                                                                                                                                                                                                                                                                                            NVVCPLQHFAKMYAQYSILQGQTGTASQGNLGWGNSGSASNSGNSQVSVYLYMFDHRASN
                                                                                                                                                                                                                                                                                                                                                                                                                                  NFMDLCSHIYFWFPMHRLLQ----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LETCV---NFVPSELADAERTAPETLEMGAK-----IKKAHVTGETPTAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FSFVPVID-----GVVFPDTPEAMLNSGNFKDTQILLGVNQNEGSYF--LIYGAPGFSKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RTVSFDEARRRAIKLGRLVGCP-DGNDTDLIDCLRSKQPQDLIDQEWLVLPF--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IYGGGFYSGSSSLDYYDGRYLAHSEKVVVVSMNYRVSAFGFLALNG-SAEAPGNVGLLDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IHGGGFIIGENHRDMYGPDYFIKKD-VVLINIQYRLGALGFLSLNSEDLNVPGNAGLKDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARDYPSACYQYVDTSYPGFSGTEMWNPNRMMSEDCLYLNVWV----
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                                                                                     FROM N.A., RRL B8079;
                                                                                                                               subtilis.
; Firmicutes;
                                                                                                                                                                           (Rel.
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                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                           30,
                                                              PubMed=7828905;
C., Swartling J
                                                                                               AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.7%;
29.9%;
                                                Swartling J., Hu
                                                                                                                                                              Last sequence update)
Last annotation update)
rase (EC 3.1.1.-) (PNB c
                                                                                                                                                                                                                                                                             609
                                                                                                                                                                                                  Created)
                                                                                                                                Bacillales;
                                                                                               SEQUENCE
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Pred. No. 3.5e-39;
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                             encoding p-1
                                                                                               OF.
                                                                                                                                Bacillaceae;
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                                                                Hodges
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                               in Escheric
                                                                                                                                                                  carboxy-esterase)
                                                                                               211-223
                                                               Pohl T.,
                                                                                                                                Bacillus
                                Escherichia
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                                                                Sutton
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SEQUENCE

OF 1-22

AND

211-223,

AND

CHARACTERIZATION

Chen Y.-R., Usui S., Yu C.-A "purification and properties subtilis.";

PDB;

1C71; 1C7J; 1QE3;

29-MAR-00.

EMBL; U06089; AAA81915.1; -. PDB; 1C71; 29-MAR-00.

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X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).

MEDLINE-20006229; PubMed-10535917;

MEDLINE-20006229; PubMed-10535917;

MEDLINE-20006229; PubMed-10535917;

Spiller B., Gershenson A., Arnold F.H., Stevens R.C.;

Spiller B., Gershenson A., Arnold F.H., Stevens R.C.;

"A structural view of evolutionary divergence.";

"A structural view of evolutionary divergence.";

"B structural view of evolutionary divergence.";

"A structural view of evolutionary divergence.";

"B structural view of evolutionary divergence.";

"A structural view of evolutionary divergence.";

"B structural view of evolutionary divergence.";

"B structural view of evolutionary divergence.";

"A structural view of evolutionary divergence.";

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IVTTQYGKVKGTT-----ENGVHKWKGIPYAKPPVGQWRFKAPEPPEVWEDVLDATAY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FIIGENHRDMY-GPDYFIKKDVYLINIQYRLGALGFLSLNSEDLNVPGNAGLKDQVMALR 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WIKNNCANFGGNPDNITTVFGESAGAASTHYMMLTEQTRGLFHRGILMSGNAICPWANTQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FYLGAGSEPLYDGSKLAAQGEVIVVTLNYRLGPFGFLHLSSFDEAYSDNLGLLDQAAALK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----GPICPQPSDLLSLSYTELPRQSEDCLYVNVFAPD-TPSQNLPVMVWIHGGA
                                                                                                                                                                                                                                                                                                                                                                                                      WVRENISAFGGDPDNVTVFGESAGGMSIAALLAMPAAKGLFQKAIMESG-ASRTMTKEQA
                                                                                                                                                                                                                          PYQTADCVLPKHPREMVKTAWGNSIPTMMGNTSYEG-LFFTSILKQMPMLVKELETCVNF
                                                                                                                                                                                                                                                                                               ASTAAAFLQVLGI----NESQLDRLHTVAAEDLLKAADQ-LKIAEKENIFQLFFQPALD
                                                                                                                                                                                                                                                                                                                                               OHRAFTLAKLAGYKGEDNDKDVLEFLMKAKPODLIKLEEKVLTLEERTNKVMFPFGPTVE
                                                                                                                                 VPSELADAERTAPETLEMGAKIKKAHVTGETPTADNFMDL------
                                                                                                                                                                                       PK----TLPEEPEKSIAEGAASGIPLLIGTTRDEGYLFFT------
                            MHRLLQLRENHTSGTPVYLYREDEDSEDLINPYRIMRSGRGVKGVSHADELTYFFWN-QL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of p-nitrobenzyl esterase from Bacillus
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696B6EF5DAA47269
                                                                                                 -YLLGK-PLAEKAADLYPRSLESQIHMMTDLLFWRP
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1.4e-37;
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----NKAFHALELPFVFGNLDG
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CRC64;
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Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9DDE3;
16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Acetylcholinesterase precursor (EC 3.1.1.7) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACES_BRARE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Zebrafish acetylcholinesterase is encoded by a single on linkage group 7. gene structure and polymorphism; and expression pattern during development."; J. Biol. Chem. 276:464-474(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE 20576389; PubMed=11016933; MEDLINE 20576389; PubMed=11016933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bertrand C., Chatonnet A., Takke Toutant J.-P., Cousin X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=7955
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AJ251640; CAC19790.1; --
HSSP; P04058; 1SOM.
ZEIN; ZDB-GENE-010906-1; ache.
                                                                                                               ACT_SITE
ACT_SITE
ACT_SITE
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR002018; Interpro; IPR000997; Interpro; IPR000379;
     DISULFID CARBOHYD
                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00878; CHOLNESTRASE.
                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                    Hydrolase;
                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00135; COesterase;
                                                                                                                                                                                                                                                                          Neurotransmitter
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LDSEITIENDPESEK 479
                                                                                                                                                                                                                                                                                                                                 PS00941;
                                                                                                                                                                                                                                                                                                                                                              PS00122;
                                                                                                                                                                                                                                                                                                          Serine esterase;
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631
                                                                                                                                                                                                                                                                                degradation;
                                                                                                                                                                                                                                                                                                                                    CARBOXYLESTERASE_B_
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                    23
634
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Cholinesterase.
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              ACETYLCHOLINESTERASE.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                             synapse; Membrane;
                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                               Glycoprotein.
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Ostariophysi; Cypriniformes;
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                                  .) (POTENTIAL).
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molecular forms
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in no way
commercial
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34

Best Local Similarity Matches 163; Conserv

Conservative

89;

Mismatches

Score 583.5; pred. No. 1.4

Query Match Best Local S

Hydrolase; ACT\_SITE CONFLICT

489 AA;

53998 MW; 19.0%;

н

pfam; pF00135; COesterase; 1
pROSITE; pS00122; CARBOXYLESTERASE\_B\_1;
pROSITE; pS00941; CARBOXYLESTERASE\_B\_2; Interpro; IPR002018; CarbesteraseB. Interpro; IPR000379; Ser\_estrs\_site.

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Serine esterase; 3D-structure.

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108 138

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168 257

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Matches
                                                                             ESTF_MYZPE STANDARD; PRT; 564 AA.

P35502;

01-JUN-1994 (Rel. 29, Created)

01-JUN-1994 (Rel. 30, Last sequence update)

01-OCT-1994 (Rel. 30, Last annotation update)

10-OCT-1994 (Rel. 30, Last annotation update)

Esterase FE4 precursor (EC 3.1.1.1) (Carboxylic-ester hydrolase)

Myzus persicae (Peach-potato aphid).

Myzus persicae (Peach-potato aphid).

Myzus persicae; Retazoa; Arthropoda; Mandibulata; Pancrustacea; Hexap

Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrh

Aphidiformes; Aphidoidea; Aphididae; Macrosiphini; Myzus.

MYBI_TaxID-13164;
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SEQUENCE FROM N.A STRAIN=Isolate 80 MEDLINE=93384534;
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:| | | :| :| | | | | | : | | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
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185; Conser
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                      .e 800F;
  PubMed-8373371;
                                             AND
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29.0%;
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                                           SEQUENCE
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Pred. No. 8e-3
92; Mismatches
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                                             OF.
                                             24 - 63
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5. 8e-37;
5. 8e-37;
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(GLCNAC.)
(GLCNAC.)
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                                                                                                                                                    Pancrustacea; Hexapoda;
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                                                                                                                                  Sternorrhyncha;
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-I- FUNCTION: OVERPRODUCTION OF NONSPECIFIC ESTERASES IS A COMMON
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CARBOXYLESTERASE_B_2;
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01-AUG-1988 (Rel. 08, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-bolinesterase precursor (EC 3.1.1.8) (Acylcholine acylhydrolase)
(Choline esterase II) (Butyrylcholine esterase)
(pseudocholinesterase)
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MEDLINE=90212557; PubMed=2322535;
Arpagaus M., Kott M., Vatsis K.P.,
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Mammalia; Eutheria; Primates;
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MEDILINE-87331856; PubMed-3035536;
Prody C.A., Zevin-Sonkin D., Gnatt A., Goldberg O.
Prody C.A., Zevin-Sonkin D., Gnatt A., Goldberg O.
Prody C.A., Zevin-Sonkin D., Gnatt A., Goldberg O.
Prody C.A., Zevin-Sonkin D., Gnatt A., Goldberg O.
Proc. Natl. Acad. Sci. U.S.A. 84:3555-3559(1987).
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  J. Biol. Chem.
                                              MEDLINE-88007487; PubMed-3115973;
Lockridge O., Adkins S., la Du B.N.;
"Location of disulfide bonds within
                                                                                                                                                                                                                                               MEDLINE-87109144; PubMed-3542989;
Lockridge O., Bartels C.F., Vaughan T.A.,
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McGuire M.C., Nogueira C.P., Bartels C.F., Lightstone H., Hajra van der Spek A.F.L., Lockridge O., la Du B.N.; and the structural mutation responsible for the "Identification of the structural mutation responsible for the dibucaine-resistant (atypical) variant form of human serum cholinesterase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bioessays 9:125-128(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [7]
REVIEW.
MEDLINE-89149758; PubMed=3067729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANT ATYPICAL GLY-98
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MEDLINE=96287386;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypocholinesterasemia.";
Hum. Mutat. 6:349-351(1995).
-i- CATALYTIC ACTIVITY: An e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Mutations of human butyrylcholinesterase
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PIR; A33769; A33769.
PIR; A33887; A33887.
PIR; A33887; A33887.
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InterPro; IPR000997; Cholinesterase.
InterPro; IPR000379; Ser_estrs_site.
                                                                                                                                                                                                                    Genew;
                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                             PRINTS; PRO0878; CHOLNESTRASE
                                                                                                                                              Pfam; PF00135; COesterase;
                                                                                                                                                                                                         MIM;
                                                                                                                  PROSITE; PS00122;
                                                                         Hydrolase; Se
Polymorphism.
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SUBUNIT: HOMOTETRAMER. THE TETRAMER OF TWO DIMERS. THE TWO SUBUNITS IN I
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TISSUE SPECIFICITY: PRESENT IN MOST CELLS EXCEPT ERYTHROCYTES.
TISSUE SPECIFICITY: PRESENT IN MOST CELLS EXCEPT ERYTHROCYTES.
DISEASE: MUTANT ALLELES OF CHEI ARE RESPONSIBLE FOR
HYPOCHOLINESTERASEMIA RESULTING IN SUXAMETHONIUM SENSITIVITY.
HYPOCHOLINESTERASEMIA RESULTING IN SUXAMETHONIUM AFTER ADMINISTRATION
HOMOZYGOUS PERSONS SUSTAIN PROLONGED APNEA AFTER ADMINISTRATION
OF THE MUSCLE RELAXANT SUXAMETHONIUM IN CONNECTION WITH SURGICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANOPHOSPHATE ESTERS. SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE {\tt SIMILARITY:}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MISCELLANEOUS: CHOLINESTERASE IS HIGHLY REACTIVE WITH
                                                                                                                                                                                                                                                                                       L; M32391; AAA99296.1; M32389; AAA99296.1; L; M32389; AAA99296.1; L; M16541; AAA98113.1; L; M16474; AAA52015.1; L; M16474; AAA52015.1; L; M16474; AAA52015.1; L; M16474; AAA52015.1; A00772; ACHU.
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CARBOXYLESTERASE_B_2; 1.
esterase; Glycoprotein;
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IN A DIMER ARE LINKED
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                             SIVKRWANFAKYGNP-
                                                                  NNAFFYYFEHRSSKLPWPEWM
                                                                                                       ILFHYTDWVDDQRPENYREALGDVVGDYNFICPALEFTKKFSEW
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                                               RMTGIWIQFATTGNPYSNEIEGMENVSWDPIKKSDEVYKCLNISDELKMIDVPEMDKIKQ
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Myzus persicae (Peach potato aphid).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha;
Aphidiformes; Aphidoidea; Aphididae; Macrosiphini; Myzus.
NCBI_TaxID=13164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND SEQUENCE STRAIN=R3 / Isolate 794J;
MEDLINE=93384534; PubMed=8373371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X74554; CAA52648.1; -. PIR; S36786; S36786.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             resistance in the peach-potato aphid, Biochem. J. 294:569-574(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1994
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InterPro; IPR000379; Ser_estrs_site.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: OVERPRODUCTION OF NONSPECIFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             carboxylic anion.
                              CCNHKDKSVQVDFITG-KVCGSEDCLYLSVYTNNLNPETK----RPVLVYIHGGGFIIGE
                                                                             ATVPGSACLGIEFGSGSKIIGQEDCLFLNVYTPKLPQENSAGDLMNVIVHIHGGGYYFGE
                                                            SASNTPKVQVHSGEIAGGFEYTYNGRKIYSFLGIPYASPPVQNNRFKEPQPVQPWLGVWN
                                                                                                                            al Similarity
167; Conser
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PS00941;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                               MEDLINE-21138439; PubMed-11239002; Wilson M.D., Riemer C., Martindale D.W., Schnucheung T.L., Hardy D.M., Schwartz S., Scherer Miller W., Koop B.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rachinsky T.L., Camp S., Li Y., Ekstroem T.J., Newton M., Rachinsky T.L., Camp S., Li Y., Ekstroem T.J., Newton M., "Molecular cloning of mouse acetylcholinesterase: tissue of alternatively spliced mRNA species."; Neuron 5:317-327(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE-90380429;
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                                                                                                                                                                                                                 "Comparative analysis of the gene-dense ACHE/TFR2 region on human chromosome 7q22 with the orthologous region on mouse chromosome 5.", Nucleic Acids Res. 29:1352-1365(2001).
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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Cell 83:503-512(1995)
                                                                                                 "Acetylcholinesterase
                                                                                                                            Bourne Y.,
                                                                                                                                              MEDLINE-96067648;
                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS)
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herer S.W.,
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InterPro; IPROUUS/, -
InterPro; IPROUUS/, -
Pfam; PF00135; COesteNeSTRASE, -
PRINTS; PRO0878; CHOLNESTERASE_B_1; 1.
PROSITE; PS00122; CARBOXYLESTERASE_B_2; 1.
PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
PROSITE; PS00941; CARBOXYLESTERASE, Synapse; Membrane; Nerve; Muscle; Signosite; PS00941; CARBOXYLESTERASE, PS00941; CARBOXYLESTERASE, PS00941; CARBOXYLESTERASE, PS00941; CARBOXYLESTERASE, PS00941; CARBOXYLESTERASE, PS00941; CARBOXYLESTERASE, PS00941; CARBOXYLESTERASE, PS00941; CARBOXYLESTERASE, PS00941; CARBOXYLESTERASE, PS00941; CARBOXYLESTERASE, PS00941; CARBOXYLESTERASE, PS00941; CARBOXYLESTERASE, PS00941; CARBOXYLESTERASE, PS00941; CARBOXYLESTERASE, PS00941; CARBOXYLESTERASE, PS00941; CARBOXYLESTERASE, PS00941; CARBOXYLESTERASE, PS00941; CARBOXYLESTERASE, PS00941; CARBOXYLESTERASE, PS00941; CARBOXYLESTERASE, PS00941; CARBOXYLESTERASE, PS00941; CARBOXYLESTERASE, PS00941; CARBOXYLESTERASE, PS00941; CARBOXYLESTERASE, PS00941; CARB
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01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Acetylcholinesterase precursor (EC 3.1.1.7) (AChE).
Torpedo californica (Pacific electric ray).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Clasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Torpediniformes; Torpedinoidei; Torpedinidae; Torpedin
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ACES_1
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Taylor
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Nature 319:407-409(1986).
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MEDLINE-88087239; Pu
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 Macphee-Quigley ., Taylor P.;
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                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS)
MEDLINE=91343928; PubMed=1678899;
Sussman J.L., Harel M., Frolow F., Oe
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"'Back door' op
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Raves M.L., Harel M.,
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                                                                                                         "Structure of acetylcholinesterase alkaloid, (-)-huperzine A."; Nat. Struct. Biol. 4:57-63(1997).
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MEDLINE-96363673; PubMed-8747462;
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Gibney G., Camp S
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                      opening implied by the crystal d acetylcholinesterase."; 38:5714-5719(1999).
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                                                           Perola
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. Dionne M., McPhee-Quigley
                                                           PubMed=10231521;
rola E., Cellai L
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., Gibney G., Rąchinsky
                                                                                                                                                                    PubMed=8989325;
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L., Silman I.,
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MEDLINE-99282167; PubMed-10353814; Millard C.B., Kryger G., Ordentlic
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Sussman J.L.;
Crystal structures of aged phosphonylated merve agent reaction products at the atomic Blochemistry 38:7032-7039(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20074924; PubMed=10606746; Silman I., Sussman J.L.; Greenblatt H.M., Kryger G., Lewis T., Silman I., Sussman J.L.; "Structure of acetylcholinesterase complexed with (-)-galanthamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEBS Lett. 463:321-326(1999).
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MEDLINE=99197295; PubMed=10368299;
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                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch)
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EMBL; X56516; .; NOT_ANNOTATED_CDS.
EMBL; X56517; ...
PIR; A00773; ACRYE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: Acetylcholine + H(2)O - choline + acetate.
SUBUNIT: THE H FORM IS AN HOMODIMER: THE ASYMMETRIC FORM IS A
DISULFIDE-BONDED OLIGOMER COMPOSED OF A COLLAGENIC SUBUNIT (Q) F
A VARIABLE NUMBER OF T CATALYTIC SUBUNITS:
A VARIABLE NUMBER OF THE H FORM IS ATTACHED TO THE MEMBRANE BY
SUBCELLULAR LOCATION: THE H FORM IS ATTACHED
                                                     [nterPro;
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ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; H/GLOBULAR (SHOWN HERE)
ALTERNATIVE PRODUCED BY ALTERNATIVE SPLICING.

AND T; ARE PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: ACHE IS FOUND IN THE SYNAPSES AND TO A LOWER
TISSUE SPECIFICITY: ACHE IS FOUND IN THE SYNAPSES AND ON
EXTERNITY IN EXTRAJUNCTIONAL AREAS OF MUSCLE AND NERVE, AND ON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTM: AN INTERCHAIN DISULFIDE BOND IS PRESENT IN WHAT BECOMES PTM: AN INTERCHAIN DISULFIDE BOND IS PRESENT IN WHAT BECOMES PTM: 1 SOFORM. POSITION 593 OF THE T ISOFORM. CARBOXYLESTERASE/LIPASE FAMILY. SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
                                                                  1CFJ; 01-APR-99.
1OCE; 18-MAY-99.
2DFP; 28-JUN-99.
1SOM; 25-JUN-99.
1DX6; 02-JAN-00.
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1FSS;
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                                                                                                                                             1EVE;
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22-MAR-99.
01-APR-99.
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31-AUG-94
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         ipR000997; Cholinesterase.
ipR000379; Ser_estrs_site.
0135; COesterase; 1.
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PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.

Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Signal; Neurotransmitter degradation; Glycoprotein; GPI-anchor; 3D-structure;
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REMOVED IN MATURE FORM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          butyrylcholinesterase
both in cat plasma.";
Biochem. Pharmacol. 60
-!- FUNCTION: RAPIDLY
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Mammalia; Eutheria;
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                                      SEQUENCE
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                                                                                                                                                                                                                                              Neurotransmitter
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                                                                                                                                                                                                                                                                                                                  InterPro; IPR002018; CarbesteraseB.
InterPro; IPR000997; Cholinesterase
InterPro; IPR000379; Ser_estrs_site
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             Match
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CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
SUBUNIT: ISOFORM H GENERATES GPI-ANCHORED DIMERS; DISULFIDE
LINKED. ISOFORM T GENERATES MULTIPLE STRUCTURES, RANGING FROM
MONOMERS AND DIMERS TO COLLAGEN TAILED AND HYDROPHOBIC-TAILED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALTERNATIVE PRODUCTS: 2 ISOFORMS; H AND T (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FORMS, IN WHICH CATALYTIC TETRAMERS ARE ASSOCIATED WITH ANCHORING PROTEINS THAT ATTACH THEM TO THE BASAL LAMINA OR TO CELL MEMBRANES. IN THE COLLAGEN-TAILED FORMS, ISOFORM T SUBUNITS ARE ASSOCIATED WITH A SPECIFIC COLLAGEN, COLO, WHICH TRIGGERS THE FORMATION OF ISOFORM T TETRAMERS, FROM MONOMERS AND DIMERS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED
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Similarity
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Chordata; Craniata; Vertebrata;
Carnivora; Fissipedia; Felidae;
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29
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Last annotation update)
precursor (EC 3.1.1.7) (AChE)
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from cat and
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Pred.
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           DB 1;
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15-JUN-2002 (Rel. 4)
15-JUN-2002 (Rel. 4)
15-JUN-2002 (Rel. 4)
Cholinesterase (EC 3)
esterase II) (Butyry
                                                                         Structure and funct pp.145-146, Plenum -!- CATALYTIC ACTIV
                                                                                                                                                                                                                                                                    BCHE
         <u>.</u>; .;
                                                                                                                                            Moorad D.R.,
"Amino acid:
                                                                                                                                                                                                                       Eukaryota; Metazoa; Mammalia; Eutheria;
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                                                                                                                                                                       TISSUE=Plasma;
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CATALYTIC ACTIVITY: An acylcholine + H(2)~ CATALYTIC ACTIVITY: An acylcholine + H(2)~ CATALYTIC ACTIVITY: An acylcholine + H(2)~ CATALYTIC ACTIVITY: An acylcholine + H(2)~ CATALYTIC ACTIVITY: HOMOTETRAMER. THE TETRAMER IS COMPOSED OF TWO SUBUNITS IN A DIMER ARE LINKED BY A DISULFIDE BOND. TISSUE SPECIFICITY: PRESENT IN MOST CELLS EXCEPT ERYTHHOUSE SPECIFICATIVE WITH
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                                                                                                                                 Doctor
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                                                                                                                             B.P., Tay
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(Rel. 41, Last sequence update)
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(Rel. 41, Last annotation update)
se (EC 3.1.1.8) (Acylcholine acylhydrolase) (Choline
(Butyrylcholine esterase) (Pseudocholinesterase) (EQ
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An acylcholine
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serum butyrycholinesterase
Quinn D.M., Rotundo R.L., G
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PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.

PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
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-!- SIMILARITY: BELONGS TO
HSSP; P21836; 1MAA.
Interpro; IPRO02018; Carbes
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                                                                                                                                                                                                                                                                                                            VDGDFLTDM-----PDTLLQLGQFKRTQILVGVNKDEGTAF--LVYGAPGFSKDNNSII-
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                                                                                                                                                                                                                                                                   FVPSELADAERT-APETLEMGAKIKKAHVTG--ETPTADNFMD----
                                                                                                     NQLAKRMPKESRBYKTIERMTGIWIOFATTGNPYSNEIEGMENVS--WDPIKKSDEVYKC
                                                                                                                                                                                     FWFPMHRLLQLRENHTSGTPVYLYRFDFDSEDLINPYRIMRSGRGVKGVSHADELTYFFW
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RX MEDLINE-2016606; pubMed-10731132; RX MEDLINE-2016606; pubMed-10731132; RA Adams M.D. Celniker S.E. Holt R.A. Evans C.A. Gocayne J.D. RA Adams M.D. Celniker S.E. Holt R.A. Holderson S.N. Amanatides P.G. Scherer S.E. Li P.M. Holderson S.N. RA George R.A. Lewis S.E. Richards S. Ashburner M. Henderson S.N. RA George R.A. Lewis S.E. Richards S. R.C. Champe M. Pfeiffer B.D. RA Sutton G.G. Wortman J.R. Yandell W.D. Zhang O. Chen L.X. RA George R.A. Lewis S.E. Helt G. Melson C.R. Miklos G.L.G. RA Balley R.M. Doyle C. Baxter E.G. Helt G. Welson C.R. Miklos G.L.G. RA Balley R.M. Doyle C. Baxter E.G. Helt G. Welson C.R. Miklos G.L.G. RA Waln K.H. Doyle C. Baxter E.G. Helt G. Welson C. Delshakov S. Beeson K.Y. Benos P.V. Berman B.P. Bhandrews Ffannkoch C. Baldwin D. RA Balley R.M. Doyle C. Baxter E.G. Helt G. Gelter A. Delshakov S. Becson K.Y. Benos P.V. Berman B.P. Bhandrews Foundari D. Bolthard A. Chandra G. L. Chandra S. Dunkov B.C. Charty J.M. Cavley S. Dahike C. Davenport L.B. Davies P. RA Cherry J.M. Cavley S. Dahike C. Davenport L.B. Davies P. M. Cavley S. Delcher A. Deng Z. Mays A.D. Dev I. Dietz S.M. RA Durbin K.J. Evangelista C.C. Ferraz G. Gebert W.M. Glasser K. RA Glodek A. Gooff F. Gorrell J.H. Gu Z. Guan P. Harris M. Harris N.L. Harvey D. Heiman T.J. Hernandez J.R. Houck J. R. Houck J. Harris N.L. Harvey D. Heiman T.J. Hernandez J.R. Houck J. Land R. A. Howland T.J. Hernandez J.R. Houck J. Land R. Lasko P. Lei Y. Levisky A.A. Li J. Li Z. Liang Y. Lin X. Lasko P. Lei Y. Levisky A.A. Li J. Li Z. Liang Y. Lin X. Lasko P. Lei Y. Levisky A.A. Li J. Li Z. Liang Y. Lin X. RA Mount S.M. Melson D. R. Murphy L. Murny D. M. Nelson D.L. RA Mount S.M. Melson N. S. Pan S. Murphy L. Murny D. M. Nelson D.L. RA Mount S.M. Melson K. A. Novanders R.D.C. Scheeler F. Shen H. RA Spier E. Spradling A.C. Stapleton M. Strong R. S. She H. Wang Z.-Y. Wassarman D.A. Weinstock G.M. Weissenbach J. M. Wang S. M. Wang S. M. Wootse S. Jan M. J. Shang S. Yao Q. D. L. R. Holley B. Wall H. Wang S. Jan M. J. Jang S. Jan X. Smith H.O. Zheng L.
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P07140; Q9VFY0;
01-APR-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ACE OR CG17907.
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Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
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"The Ace locus of Drosophila
acetylcholinesterase with an
EMBO J. 5:2949-2954(1986).
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CONFLICT
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CARBOHYD
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InterPro; IPR000997; Cholinesterase.
InterPro; IPR000379; Ser_estrs_site.
Pfam; PF00135; COesterase; 1.
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PIR; A33469; A33469.
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*Acetylcholinesterase from Drosophila
two subunits encoded by the same gene.
FEBS Lett. 238:333-337(1988).
                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                        CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: Acetylcholine + H(2)0 - choline + acetal SUBUNIT: THE ACTIVE ENZYME SEEMS TO BE COMPOSED OF THE NON-COVALENT ASSOCIATION OF A 55 KDA AND A 16 KDA POLYPEPTIDE. ACTIVE UNITS ARE LINKED TOGETHER BY A DISULFIDE BOND AT THE TERMINUS OF THE 55 KDA PEPTIDE.
SUBCELLULAR LOCATION: LINKED TO THE MEMBRANE OF THE NEURONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced through a ween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: LINKED TO THE MEMBRANE OF THE NEURONAL CHOLINERGIC SYNAPSES BY A GPI-ANCHOR.
SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DRLVVQTSSGPVRG-RSVTVQGREVHVYTGIPYAKPPVEDLRFRKPVPAEPWHGVLDATG
                    AE003699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X05893; CAA29326.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PR00878; CHOLNESTRASE.
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an email to license@isb-sib.ch).
                                                                                          Similarity
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PubMed=1730712;
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3; Mismatches
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01-OCT-1994
01-OCT-1994
15-JUN-2002
acetylcholinesterase.";
FEBS Lett. 315:163-166(1993).
-i- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
-i- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
-i- SUBUNIT: OLIGOMER COMPOSED OF DISULFIDE-LINKED HOMODIMERS.
-CATALYTIC FORMS H (GPI-ANCHOR DIMER) AND T (ASYMMETRIC COLLAGE)
                                                                                                                                            [2.
                                                                                                                                                      generation of multiple molecular
Torpedo collagenic subunit.";
J. Neurochem. 60:337-346(1993).
                                                                                                           SEQUENCE FROM N.A. MEDLINE=93114454;
                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; CBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                            01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Acetylcholinesterase precursor (EC 3.1.1.7) (
                                                                                  "Expression of a cDNA encoding
                                                                                                                                                                                                                             MEDLINE=93107932;
                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
                                                                                                 Legay C.,
                                                                                                                                                                                                 Legay C., Bon S., Vernier P., Coussen F., Massoulie J.;
*Cloning and expression of a rat acetylcholinesterase subunit:
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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PubMed=8417155;
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EMBL; $70140; CAA49717.1; --
EMBL; $70141; CAA49718.1; --
PIR; JH0811; JH0811.
HSSP; P21836; 1MAA.
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PROSITE; PS00122; CARBOXYLESTERASE_B_2; 1
PROSITE; PS00941; CARBOXYLESTERASE, Synapse; Membrane; Nerve; Mu
Hydrolase; Serine esterase; Synapse; Membrane; Alternative
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InterPro; IPR000997; Cholinesterase.
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OF KNOWN ACHE FORMS:

ALTERNATIVE PRODUCTS: 3 isoforms; T (shown here), H produced by alternative splicing. It is not known wl R is functional.

R is functional.

R IS functional.

R IS FUNCTIONAL NERVOUND IN CENTRAL NERVOUND SUPERINGER BUT NOT TIVED.
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                                                                                                          GPDYFIK-KDVVLINIQYRLGALGFLSLNSEDLNVPGNAGLKDQVMALRWIKNNCANFGG
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                                                                                                                                                                DFITGKVCG-----SEDCLYLSVYTNNLNPETKRPVLVYIHGGGFIIGENHRDMY 148
                                                                                                                                                                                             GQLRGI-RLKAPGGPVSAFLGIPFAEPPVGSRRFMPPEPKRPWSGILDATTFQNVCYQYV
KLAGYK---GEDNDKDVLEFLMKAKPQDLIKLEEKVLTLEERTNKVMFPFGPTVEPYQTA
                           NPDNITVFGESAGAASTHYMMLTEQTRGLFHRGILMSGNAICPWANT---QCQHRAFTLA
                                                                                DGRFLAQVEGTVLVSMNYRVGTFGFLALPG-SREAPGNVGLLDQRLALQWVQENIAAFGG
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P23795; 097579;
01-NOV-1991 (Re
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-98359754; PubMed-9693127; Mendelson I., Kronman C., Ariel N., Shafferman A., "Bovine acetylcholinesterase: cloning, expression characterization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND CHARACTERIZATION
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                              -!- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
-!- FUNCTION: RAPIDLY HYDROLYZES CHOLINE + H(2)O = choline + acetate.
-!- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
-!- SUBUNIT: ISOFORM H GENERATES GPI-ANCHORED DIMERS; DISULFIDE
-!- SUBUNIT: ISOFORM T GENERATES MULTIPLE STRUCTURES, RANGING FROM
MONOMERS AND DIMERS TO COLLAGEN-TAILED AND HYDROPHOBIC-TAILED
MONOMERS AND DIMERS TO COLLAGEN-TAILED AND HYDROPHOBIC-TAILED
FORMS, IN WHICH CATALYTIC TETRAMERS ARE ASSOCIATED WITH ANCHORING
FROTEINS THAT ATTACH THEM TO THE BASAL LAMINA OR TO CELL
PROTEINS THAT ATTACH THEM TO THE BASAL LAMINA OR TO CELL
MEMBRANES. IN THE COLLAGEN TAILED FORMS, ISOFORM T SUBUNITS ARE
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ASSOCIATED WITH A SPECIFIC SOLLAGEN, COL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=90306335; PubMed=2365060;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     cholinesterases."
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                                                                                                  SIMILARITY:
  European Bioinformatics
SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.

PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.

Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Muscle; Neurotransmitter degradation; Glycoprotein; Alternative splici
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF061815; AAC64270.1;
EMBL; AF061813; AAC64270.1;
EMBL; AF061814; AAC64270.1;
PIR; S10712; S10712.
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InterPro; IPR000997; Cholinesterase.
InterPro; IPR000379; Ser_estrs_site.
Pfam; PF00135; COesterase; 1.
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GlycoSuiteDB; P23795; -.
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DCVLPKHPREMVKTAWGNSIPTMMGNTSYEGLFFTSILKQMPMLVKELETCVNFVPSELA
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                                                                                KLAGYK----GEDNDKDVLEFLMKAKPQDLIKLEEKVLTLEERTNKVMFPFGPTVEPYQTA
                                                                                                                                      DPTSVTLFGESAGAASVGMHLLSPPSRGLFHRAVLQSGAPNGPWATVGVGEARRRATLLA
                                                                                                                                                            NPDNITVFGESAGAASTHYMMLTEQTRGLEHRGILMSGNAICPWANT---QCQHRAFTLA
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L -> W (IN REF 2).

C -> A (IN REF 2).

EVRRCL -> GVPQAS (IN S -> N (IN REF 2).
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Pred. No. 2.7e-35;
4; Mismatches 229;
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                                                                                           HTSGTPVYLYRFDFDSEDLINPYRIMRSGRGVKGVSHADELTYFFWNQLAKRMPKESREY
                                                                                                                                            GVRVGVPQASDLAAEAVVLHYTDWLHPEDPARLREALSDVVGDHNVVCPVAQLAGRLA--
                                                                                                                                                                        DAERTAPETLEMGAKIKKAHVTG----ETPT--ADNFMDLCSHIYFWFPMHRLL-QLRFN 434
                                                                                                                                                                                                               DT----PEALINAGDFHGLQVLVGVVKDEGSYF--LVYGAPGFSKDNESLISRA-QFLA
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Search completed: April 4, 2003, 09:13:36
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2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
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6: sp_mammal:*
7: sp_mhc:*
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9: sp_bhage:*
10: sp_plant:*
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sp_mammal:*
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esult No.	Score	Query Match	Length	DB	ID	Description
_	3073	100.0	570	5	Q25252	Q25252 lucilia cup
2	2431	79.1	570	σ	Q9XZ70	musca do
w	2348	76.4	570	σ	Q9U4U9	Q9u4u9 haematobia
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ъ	1966.5	64.0	556	ر.	Q24201	Q24201 drosophila
6	1412.5	46.0	567	IJ	Q9VIB3	
7	1411.5	45.9	558	ر ح	Q24202	
œ	1408.5	45.8	554	σ	Q9VIB0	
9	1389.5	45.2	572	ۍ	Q9VIB1	Q9vibl drosophila
10	1378.5	44.9	572	თ	Q24203	
11	1353.5	44.0	565	σ	Q9NI59	_
12	1330.5	43.3	566	ഗ	Q961N0	Q961n0 drosophila
13	1324.5	43.1	554	u	Q9VIC2	
14	1322.5	43.0	554	v	Q24195	
15	1306.5	42.5	564	v	Q9NI61	
16	1302.5	42.4	566	5	Q9W243	

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Q23736	P91598	Q9ni60	P91596	P91597	Q9vib6	Q9ni58	Q24197	Q9vic0	Q23735	Q23734	P91920	Q9gu95	Q9ni55	σ		Q9vic1	. 023733	Q8wq88	P92025	Q8wq89	Q91715	Q24198	Q24204	Q9vib9	Q95u30	Q9ni53	Q24194	COTAGN
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STRAIN-RUTGERS DIAZINON-R;
MEDLINE-99381228; PubMed-10451921;
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Muscoidea; Muscidae;
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Eukaryota; Metazoa; Arthropoda;
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                           Pfam: PF00135; COesterase; PROSITE; PS00122; CARBOXYL Hydrolase.
                                                                                                                  InterPro; IPR002018; CarbesteraseB. InterPro; IPR000379; Ser_estrs_site
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            AA;
                                                                       CARBOXYLESTERASE_B_1;
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Musca.
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12, Last sequence update)
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                                                                                        PROSITE; F
Hydrolase.
SEQUENCE
STRAIN-BERKELEY;

MEDLINE-20196006; PubMed-10731132;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer

Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.
                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                               FWYPMHRFLQLRFNHTVGSPIYLYRFDFDSEEIINPYRIMRYGRGVKGASHTDELTYLFW
                                                                                                                                                                                                                                                                                                                                                                                      EELRDKVMFAFGPTTEPYETPDCVLPKPNREMLKTAWGNSIPTLIGNTSYEGLLFISVGK
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73.9%;
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Pred. No. 3
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                                                                                                                     Hexapoda;
                                                                                                                                                          update)
                                                                                                            Brachycera;
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RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Ferriac C., Ferriaca S., Pleischmann W.,
RA Glasser K., Gorge F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kannison J.A., Ketchum K.A.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kannison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pecleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pecleb J.M.,
RA Rinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Suriskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Yella M., Mand M., Shang G., Zhao Q., Zheng L.,
RA Shen B., Shang G., Shang M., Venter J.C
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Best Local S
Matches 365
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Champe M., Chavez C., Dorsett V., Farfan D., Frise
A Gonzalez M., Guarin H., Li P., Liao G., Miranda A.,
Nunco J., Pacleb J., Paragas V., Park S., Phoudanen
Yu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ datal
-!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTEI
EMBL; AB003671; AAF54010.1; -
EMBL; AF051473; AAF54010.1; -
EMBL; AF051473; AAF54010.1; -
EMBL; AF051836; IMAA
FlyBase; FB900015575; alpha-Est7
InterPro; IPR000379; Ser_estrs_site.
Pfam; PF00135; Coesterase; 1.
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Hydrolase.
SEQUENCE
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   181
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                                 NVPGNAGLKDQVMALRWIKNNCANFGGNPDNITVFGESAGAASTHYMMLTEQTRGLFHRG
                                                                                                                        MNFNVSLMEKLKWKIKCIENKFLNYRLTTNETVVAETEYGKVKGVKRLTVYDDSYYSFEG
   NVPGNAGLKDQVLALKWIKNNCASFGGDPNCITVFGESAGGASTHYMMLTDQTQGLFHRG
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                                                                                                                                                                                                                                                                                      IPYAQPPVGELREKAPQRPTPWDGVRDCCNHKDKSVQVDFITGKVCGSEDCLYLSVYTNN
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64.0%;
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Pred. No. 7.3e
91; Mismatches
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CARBOXYLESTERASE/LIPASE FAMILY
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D., Frise E., George R.,
iranda A., Mungall C.J.,
Phouanenavong S., Wan K
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Best Local S
Matches 359
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;
Pterygota; Neoptera; Endopterygota; Diptera; Brachyce
Ephydroidea; Drosophilidae; Drosophila.
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ALPHA-EST7 OR AE7 OR CG1112.
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    421
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Interpro; IPR000379; Ser_estrs_site.
Pfam; PF00135; COesterase; 1.
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  198
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                                                                                                                                                                                                      RPIPWEGVRDCSQPKDKAVQVQFVFDKVEGSEDCLYLNVYTNNVKPDKARPVMVWIHGGG
                                                                                                                                          RPTPWDGVRDCCNHKDKSVQVDFITGKVCGSEDCLYLSVYTNNLNPETKRPVLVYIHGGG
                                                                                                                                                                                                                         IENKELNYRLTYNETVVAETEYGKVKGVKRLTVYDDSYYSFEGIPYAQPPVGELRFKAPQ
IKNNCANFGGNPDNITVFGESAGAASTHYMMLTEQTRGLFHRGILMSGNAICPWA-NTQC
                                        FIIGENHRDMYGPDYFIKKDVVLINIQYRLGALGFLSLNSEDLNVPGNAGLKDQVMALRW
                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                    556 AA;
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                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOXYLESTERASE_B_1;
                                                                                                                                                                                                                                                                                                                                                                    556
63397 MW;
                                                                                                                                                                                                                                                                                                           64.0%;
                                                                                                                                                                                                                                                                                            85;
                                                                                                                                                                                                                                                                                                                 Pred.
                                                                                                                                                                                                                                                                                                               score 1966.5; DB 5; Length
pred. No. 1.5e-154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                         AF0F80A1D3C34425 CRC64;
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          RESULT
Q9VIB3
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RX MEDLINE=20196006; PubMed=10/3114;
RA Addams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Addams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Addams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Addams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Addams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Champe M., Pfeiffer B.D.,
RA George R.A., Lewis S.E., Richards G., Champe M., Pfeiffer B.D.,
RA George R.A., Lewis S.E., Randell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., Baxendale J., Belsonkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bahndari D., Belshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Gorkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Dourbin K.J., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Glodek A., Gong F., Downes M., Dugann Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Degwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Degwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Liang Y., Lin X.,
RA Hostin D., McIntosh T.C., McLeod M.P., McPherson D.L.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.P., Moshref D., Muzphy L., Muzny D.M., Nelson D.L.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9VIB3;
Q9VIB3;
01-MAY-2000
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01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alpha-EST8 protein.
ALPHA-EST8 OR CG1121.
ALPHA-EST8 OR CG1121.
Drosophila melanogaster (Fruit fly).
Brosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Metazoa; Arthropoda; Diptera; Brachycera; Muscomorpha;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSELADAERTAPETLENGAKİKKAHVTGETPTADNFMDLCSHIYFWFPMHRLLQLRFNHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGTPVYLYRFDFDSEDLINPYRIMRSGRGVKGVSHADELTYFFWNOLAKRMPKESREYKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGAPVYFYRYDFDSEELIFPYRIMRMGRGVKGVSHADDLSYQFSSLLARRLPKESREYRN
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Last sequence update)
Last annotation update)
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Best Local Similarity
Matches 267; Conser
 Q24202
Q24202;
Q1-NOV-1996
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-I- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMERSED 237657. 10E3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P37967; 1QE3.

FlyBase; FBgn0015576; alpha-Est8.
InterPro; IPR002018; CarbesteraseB.
InterPro; IPR00379; Ser_estrs_site.
Pfam; PP00135; COesterase; 1.
PROSITE; PS00122; CARBOXYLESTERASE_B_1;
PROSITE; PS00941; CARBOXYLESTERASE_B_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reinert K.,
                                                                      555
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                                                                                                                                                                                                                                                                        QATGYTGDANDRDIFAHLKKCKASSMLKVAEDIITMEERHQRLTMFSFGPTIEPYLTPHC
                                                                                                                                                                                                                                                                                   GGNPDNITVFGESAGAASTHYMMLTEQTRGLEHRGILMSGNAICPWANTQCQ-HRAFTLA
                                                                                                                                                                                                                                                                                                                                                                 DMYGPDYFIKKDVVLINIQYRLGALGFLSLNSEDLNVPGNAGLKDQVMALRWIKNNCANF
                                                                                                                                                                                                                                                                                                                                                                                                                                     RLTTNETVVAETEYGKVKGVKRLTVYDDSYYSFEGIPYAQPPVGELRFKAPQRPTPWDGV
                                                                     RLWDCIYDR
                                                                                        KQWESMFEK
                                                                                                           VSMVVHFAISGDPNIPMVCQDEKEQPRGAWLPISKDDKVFQCLNISHDVHVIDLPEAEKL
                                                                                                                              TGIWIQFATTGNP----YSNEIEGMENVSWDPIKKSDEVYKCLNISDELKMIDVPEMDKI
                                                                                                                                                 TFLYRFDFDSKH-FNIMRIITCGRKVRGTCHADDLSYLFYNAAAKKLKRRTAEFKTIKRL
                                                                                                                                                                                         HVDEQQRKAFGKKVRELYFGDRTPGRKTILEYSDLFSYKYFWHGIHRTLLSRAHHAPLAP
                                                                                                                                                                                                      ERTAPETLEMGAKIKKAHVTGETP----TADNFMDLCSHIYFWFPMHRLLQLRFNHTSGTP
                                                                                                                                                                                                                                 VIPKSPLEMMRDCWGNSIPMVIGGNSFEGLLMFPEVNKWPELLCQLGDCENLAPQ---
                                                                                                                                                                                                                                                                                                               GGDPDNITVFGESAGGASTHYMMLTDQAKGLFHKTIIMSGSALAPWAQTPTHINWPYRLA
                                                                                                                                                                                                                                                                                                                                                      DLYSPDYIMMEHVVLVVISYRLGALGFLSLADEELDVPGNAGLKDQVMALRWVKRNCQFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     567
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 (TrEMBLrel. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                        565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64831 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.0%; Score 1412.5; DB 5;
48.6%; Pred. No. 1.4e-108;
Live 105; Mismatches 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saunders R.D.C.,
 Created)
                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07D6ACC72786F14A CRC64;
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Smith H.O
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Query Match
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01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Alpha esterase (Fragment).
ALPHA-EST8 OR CG1121.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscc Ephydroidea; Drosophilidae; Drosophilia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U51052; AAB01151.1; -.
HSSP; P37967; 1QE3.
FlyBase; FBgn0015576; alpha-Est8.
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J. Mol. Evol. 0:0-0(0).
-!- SIMILARITY: BELONGS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00122; CARBOXYLESTERASE_B_1; PROSITE; PS00941; CARBOXYLESTERASE_B_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002018; CarbesteraseB.
InterPro; IPR000379; Ser_estrs_site
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NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RLTINETVVAETEYGKVKGVKRLTVYDDSYYSFEGIPYAQPPVGELRFKAPQRPTPWDGV
                                                                                                                                                                                           VYLYRFDFDSEDLINPYRIMRSGRGVKGVSHADELTYFFWNQLAKRMPKESREYKTIERM
                                                                                                                                                                                                                                                                                                                                                                                               QATGYTGDANDRDIFAHLKKCKASSMLKVAEDIITMEERHQRLTMFSFGPTIEPYLTPHC
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                                   KOWESMFEK 565
                                                                                                             TGIWIQFATTGNP----YSNEIEGMENVSWDPIKKSDEVYKCLNISDELKMIDVPEMDKI 556
                                                                                                                                                                                                                                    HVDEQQRKAFGKKVRELYFGDRTPGRKTILEYSDLFSYKYFWHGIHRTLLSRAHHAPLAP
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                                                                                                                                                                                                                                                                                                              VIPKSPLEMMRDCWGNSIPMVIGGNSFEGLLMFPEVNKWPELLCQLGDCENLAPQ---DA
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                                                                        VSMVVHFAISGDPNIPMVCQDEKEQPRGAWLPISKDDKVFQCLNISHDVHVIDLPEAEKL
                                                                                                                                                        TFLYRFDFDSKH-FNIMRIITCGRKVRGTCHADDLSYLFYNAAAKKLKRRTAEFKTIKRL
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Pred. No. 1.7
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RX MEDLINE-ZU196006; PubMed-10731132;

RA Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., RA Amanatides P.G., Scherer S.E., Richards S. Ashburner M., Henderson S.N., Gorge S. H.C., Blazej R.G., Champe M., Pfelifer B.D., RA Brandon R.C., Mogers Y.H.C., Blazej R.G., Champe M., Pfelifer B.D., RA Brandon R.C., Mogers Y.H.C., Blazej R.G., Champe M., Pfelifer B.D., RA Ballew R.M., Basu A., Baxter E.G., Helt G., Welson C.R., Miklos G.L.G., RA Ballew R.M., Basu A., Baxter E.G., Helt G., Welson C.R., Miklos G.L.G., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroju L., Beasley E.M., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroju L., Beasley E.M., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroju L., Beasley E.M., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroju L., Beasley E.M., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroju L., Beasley E.M., RA Ballew R.M., Basu A., Bouck J., Brokstein P., Brottier P., RA Ballew R.M., Basu A., Bouck J., Brokstein P., Brottier P., RA Ballew R.M., Calays S., Dahlke C., Davenport L.B., Davies P.M., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.M., RA Bartis M., RA Gladek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Gladek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Gladek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Gladek A., Gong F., Karpen G.H., Ke Z., Kennison J.A., Houck J., RA Harris N.L., Harvey D., Helman T.J., Wel M.-H., Ibegwam C., RA Mentilov G., Mishina N.V., Mobarry C., Morris J., Woshrefi A., Lia X., Mattel B., McIntosh T.C., McLeod M.P., Mepherson D.L., Ra Merkilov G.M., Mishina N.V., Mobarry C., Morris J., Woshrefi A., Shue B.C., Siden-Kiamos I., Slanders R.D.C., Schepler F., Shen H., Ra Shue B.C., Siden-Kiamos I., Slanders R.D.C., Schepler F., Shen H., Ra Shue B.C., Siden-Kiamos I., Slanders R.D., Mary S., Mang A.H., Wang A.H., Wang A.H., Wang A.H., Wang A.H
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01-MAY-2000 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alpha-EST9 protein.
ALPHA-EST9 DR CG1128.
ALPHA-EST9 DR CG1128.
Drosophila melanogaster (Fruit fly).
Brosophila melanogaster (Fruit fly).
Eukatyota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukatyota: Metazoa; Arthropoda; Diptera; Brachycera; Muscomorpha;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                           -i- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY EMBL; AE003671; AAF54014.1; -. HSSP: B379671; 10E3.
                                                                                                                                                                                                       FlyBase; FBgn0015577; alpha-Est9
                                                                                              Hydrolase.
SEQUENCE
                                                                                                                        PROSITE; PS00122; CARBOXYLESTERASE_B_1;
                                                                                                                                      Pfam; PF00135; COesterase; 1.
PRINTS; PR00878; CHOLNESTRASE.
              18
Similarity
                                                                                                                                                                 IPR0000997; Cholinesterase.
IPR000379; Ser_estrs_site.
                                                                                                                                                                                           IPR002018; CarbesteraseB
                                                                                                 554 AA;
                                           Conservative
                                                                                                 63670
                                                        45.8%;
48.5%;
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                                           Score 1408.5; DB
pred. No. 3e-108;
95; Mismatches 178
                                                                                                    0A72368389DFFC2B CRC64;
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В
RX MEDLINE-20196006; pubMed-10731132;
RX MEDLINE-20196006; pubMed-10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Gorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Pfeiffer B.D.,
RA George R.A., Lewis S.E., Randell M.D., Zhang Q., Chen L.X.,
RA George R.A., Lewis S.E., Randell M.D., Zhang Q., Chen L.X.,
RA George R.A., Lewis S.E., Randell M.D., Zhang Q., Chen L.X.,
RA George R.A., Lewis S.E., Randell M.D., Zhang Q., Chen L.X.,
RA Wan K.H., Dayle C., Bayter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Dayle C., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Deva I., Dletz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
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01-MAY-2000 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musco
Ephydroidea; Drosophilidae; Drosophila.
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ALPHA-EST9 OR CG1128.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
RA Syirs E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Rubin G.M., Venter J.C.;
RT The genome sequence of Drosophila melanogaster.";
RT Similarity: Belongs To THE Type-B CARBOXYLESTERASE/Lipase FAMILY.
DR HSSP; P37967; 10E3.
DR F19Base; FB9n0015577; alpha-Est9.
DR Interpro. TPRD07118. Carboeterasen
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PRINTS; PR00878; CHOLNESTRASE.
PROSITE; PS00122; CARBOXYLESTERASE_B_1;
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YFFWNQLAKRMPKESREYKTIERMTGIWIQFATTGNP-YSNEIEGMENVSW---
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Query Match
Best Local S
Matches 267
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01-NOV-1996
01-JUN-2002
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Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Robin C., Medveczky K.M., Russell
J. Mol. Evol. 0:0-0(0).
-: SIMILARITY: BELONGS TO THE TY
EMBL; U51053; AABOL152.1; -.
HSSP; P37967; 1QE3.
ElyBase; FB900015577; alpha-Est9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002018; CarbesteraseB.
InterPro; IPR000379; Ser_estrs_site
Pfam; PF00135; Coesterase; 1.
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ALPHA-EST9 OR AE9 OR CG1128
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                                                                                                              KQMPMLVKELETCVNFVPSELADAERTAPETLEMGAKIKKAHVTGETPTAD---NFMDLC
                                                                                                                                                                             LEERTNKVMFPFGPTVEPYQTADCVLPKHPREMVKTAWGNSIPTMMGNTSYEGLFFTSIL
                                                                                                                                                                                                                                       GILMSGNAICPWANTQCQHRAFTLAKLAGYKGEDNDKDVLEFLMKAKPQDLIKLEEKVLT
                                                                                                                                                                                                                                                                                      FQFGEASRECYSPDYLLREDVVVISINYRLGPLGTNDDTWKKKHIFNISLPGFLCLDDPE
                                                                                                                                                                                                                                                                                                                                                                      FIIGENHRDMYGPDYFIKKDVVLINIQYRLGAL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VDFKVQQRRYRTSEKTVVSTTYGPIKGVKRKSIYGQSYFSFERIPFAKPPVGDVRYKAPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IENKFLNYRLTTNETVVAETEYGKVKGVKRLTVYDDSYYSFEGIPYAQPPVGELRFKAPQ
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YFFWNQLAKRMPKESREYKTIERMTGIWIQFATTGNP-YSNEIEGMENVSW----DPIKKS
                              SHEYFWFPIYRTVLSRLQYARSAPTYLYRFDFDSKH-FNHLRILSCGKKVRGTCHGDDLS
                                                            SHIYFWFPMHRLLQLRFNHTSGTPVYLYRFDFDSEDLINPYRIMRSGRGVKGVSHADELT
                                                                                                                                                           DEEKKERIGFSFGPVIEPYVTSHCVVPKKPIEMMRTAWSNNIPLTIGGVSNEGLLLYSET
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267; Conserv
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Pred. No. 9.7e-
96; Mismatches
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Best Local Similarity
Matches 255; Conserv
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Q961N0;
Q1-DEC-2001 (TIEMBLrei
Q1-DEC-2001 (TIEMBLrei
Q1-JUN-2002 (TIEMBLrei
Q1-JUN-2002 (TIEMBLrei
QH15053P,
ALPHA-EST2 OR CG2505.
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-- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
-- EMBL, AV051497; AAK92921.1; --
EMBL, AV051497; AAK92921.3; --
EMBL, AV051497; AAK92921.3; --
EMBL, AV051497; AAK92921.5; --
EMBL, AV051497; Carbesteraseb.
InterPro; IPR000379; Ser_estrs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;
Eterygota; Neoptera; Endopterygota; Diptera; Brachyce
Ephydroidea; Drosophilidae; Drosophila.
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NCBI_TaxID=7227;
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SEQUENCE
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                                                                                                                                                                                                                                                                                       MNENVSLMEKLKWKIKCIENKELNYRLTTNETVVAETEYGKVKGVKRLTVYD-DSYYSEE 59
                                                                                                                                                                                                       NLNPETKRPVLVYIHGGGFIIGENHRDMYGPDYFIKKDVVLINIQYRLGALGFLSLNSED
                                                                                                                                                                                                                                          GIPYAQPPVGBLREKAPQRPTPWDGVRDCCNHKDKSVQVDEITGKVCGSEDCLYLSVYTN 119
                                                                                                                                                                                       KQMPMLVKELETCVNFVPSELADAERTAPETLEMGAKIKKAHVTGETPTADNF----
                                                           LEERTNKVMFPFGPTVEPYQTADCVLPKHPREMVKTAWGNSIPTMMGNTSYEGLFFTSIL
                                                                                     AIMQSGCALSEWVESPDNNWAFRLAQNLGYKGDEKDADVLSFLSKVCARQIAAIDQDVIN
                                                                                                  LNVPGNAGLKDQVMALRWIKNNCANFGGNPDNITVFGESAGAASTHYMMLTEQTRGLFHR
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                                     LDEVRSTLLFAFGPVIEPYETDHCVVPKRHKDLLSEAWGNDIPVIVGGNSFEGLFSYQLV
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l (TrEMBLrel.
l (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                             566 AA;
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                                                                                                                                                                                                                                                                                                                                            Conservative 115;
                                                                                                                                                                                                                                                                                                                                                                                               64664 MW;
                                                                                                                                                                                                                                                                                                                                                        43.3%; Score 1330.5;
44.7%; Pred. No. 9.26
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19,
21,
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Mismatches 187; Indels
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                      MDLC
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                       416
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Query Match Best Local S Matches Q9NI59; 01-OCT-2000 01-OCT-2000 01-JUN-2002 Drosophila buzzatii (Fruit fly). Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. NCBI\_TaxID=7264; Q9NI59 Alpha-esterase 2. AE2A OR AE2. HSSP; P37967; 1QE3. FlyBase; FBgn0029452; Dbuz\aE2a. InterPro; IPR002018; CarbesteraseB.
InterPro; IPR000397; Cholinesterase.
InterPro; IPR000379; Ser\_estrs\_site Pfam; PF00135; 190 190 130 130 250 250 11 LKWKIKCIENKELNYRLTINETVVAETEYGKVKGVKRLTVYDDSYY-SFEGIPYAQPPVG 310 10 70 70 KHQLKCLNISDELKVIDVPDLKKLMVWESFFRR LVYIHGGGFIIGENHRDMYGPDYFIKKDVVLINIQYRLGALGFLSLNSEDLNVPGNAGLK 189 ELRERAPOPPDPWKGVRNCTTYGOKPLORNMVMGLIEGSEDCLYLNVYSKSLRTENPLPV ELREKAPORETPWDGVRDCCNHKDKSVQVDETTGKVCGSEDCLYLSVYTNNLNPETKRPV 129 AWADTPORNWALRLAROMGYKGTDSEEDILRYLTKASARQIASHDQEIVTLDEFRNFYLY PWANTQCQHRAFTLAKLAGYKGEDNDKDVLEFLMKAKPQDLIKLEEKVLTLEERTNKVMF H---NIIPREV--SESSTPEQLEQLVRRLKQLYFGDEQRECMKLFEALDIFSHRQIWHDL AFGPIVEDYESEHCVVPKPHKEMLATAWGNSLPLIVGGNSFEGLFSYQLVRNDPWVMTNF PFGPTVEPYQTADCVLPKHPREMVKTAWGNSIPTMMGNTSYEGLFFTSILKOMPMLVKEL HRLLQLRENHTSGTPVYLYREDEDSEDLINPYRIMRSGRGVKGVSHADELTYFFWNQLAK ETCVNEVPSELADAERTAPETLE-MGAKIKKAHVTGETPTADNF---MDLCSHIYFWFPM PR00878; CHOLNESTRASE. Similarity (TrEMBLIE) (TrEMBLIE) 565 PRELIMINARY; Conservative AA; COesterase 64618 MW; 44.0%; Score 1353.5; 1 46.2%; Pred. No. 1.1e-15, 15, 21, 110; Last sequence update)
Last annotation update) Created) OBC92E956B23006E CRC64; Mismatches 170; 568 Ą DB 5; Indels Length 25; FAMILY Gaps 189 69 69 129 249 249 485 425 369 309 424 369 9.

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        RA Adams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Hil P.W., Hoskins R.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Hil P.W., Hoskins R.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Hilmand S., Ashburner M., Henderson S.N.,
RA Bandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Becson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Bötchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan A.E., Bouck J., Brokstein P., Davles P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA Glodek A., Goop F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Glodek A., Goop F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Glodek A., Goop F., Gorrell J.H., Gu Z., Kennison J.A., Ketchum K.A.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hount S.M., Moy M., Murphy L., William P., Harris M.,
RA Harris N.L., Harvey D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Murzny D.M., Nelson D.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Smith T.,
RA Sheng X.H., Zhong W., Zhou W., Zhu S., Zhu X., Smith H.O.,
RA The genome sequence of Drosophila melanogaster.";
RL Schence 287:1218 APS4003 1.
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Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
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ALPHA-EST2 OR CG2505.
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MEDLINE=20196006;
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RESULT 14
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AC Q2419
AC Q2419
AC DT 01-NC
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DE Alpha
GN ALPHA
GN ALPHA
OC Dreary
OC Eukax
OC Ptery
OC Ephyd
OX NCBL]
RP SEQUE
RA RObin
RL J. MC

ALPHA-EST2 OR A

01-NOV-1996 (TrEMBLrel. 01-NOV-1996 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel.

01, 01, 21,

Created)

Last sequence update)
Last annotation updat

update)

Q24195 Q24195;

PRELIMINARY;

554

ALPHA-EST2 OR AE2 OR CG2505.

Drosophila melanogaster (Fruit fly).

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.

NCBI\_TaxID=7227;

Hexapoda; Insecta;

Brachycera;

Muscomorpha;

SEQUENCE FROM Robin C., Medv. J. Mol. Evol.

Medveczky K.M.,
vol. 0:0-0(0).

Russell

R.J.,

Oakeshott

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FlyBase; FBgn0015570; alpha-Est2.
InterPro; IPR002018; CarbesteraseB.
InterPro; IPR000997; cholinesterase.
InterPro; IPR000379; Ser_estrs_site.
Pfam; pF00135; COesterase; 1.
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SDCLAVWDTFYPR
                         MDKIKQWESMFEK
                                                                  YKTIERMTGIWIQFATTGNPYSNEIEGMENVSWDPIK-KSDEVYKCLNISDELKMIDVPE
                                                                                                      SYAPKTETYLYRFOFDSPH-FNQFRRLVCGDRIRGVAHADELSYLFYNIIASKLDKSSME
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                                                                                                                                                              PREVRETSSLEGQDL-LVRRLKQLYFNNEMQESMEMFEALNIFSHRQIWHDTHRFILARQ
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                                                    YKTIERMYGMWTSFASSGNPNCPE---LGSAKWEAVQLKENAVEKCFNISHDLEMRDLPE
                                                                                                                                                                                    PSELADAERTAPETLEMGAKIKKAHVTGETPTADNF----MDLCSHIYFWFPMHRLLQLRF
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8; CHOLNESTRASE.
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Matches 252
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InterPro; IPR002018; CarbesteraseB.
InterPro; IPR000379; Ser_estr5_site.
Pfam; pr00135; Coesterase; 1.
HydroLese.
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01-OCT-2000 (TrEMBLrel. 1
01-OCT-2000 (TrEMBLrel. 1
01-JUN-2002 (TrEMBLrel. 2
Alpha-esterase la.
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                                              Drosophila buzzatii (Fruit fly).
Drosophila buzzatii (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Inse
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
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SEQUENCE FROM N.A.
Robin C., Claudianos
"The alpha-esterase
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                                                                                                                                              PRELIMINARY;
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                                                                                                        Created)
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ila buzzatii.";
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-i- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
EMBL; AF216208; AAF26721.1; -.
HSSP; P37967; 10E3.
FlyBase; FB900029453; Dbuz\aEla.
InterPro; IPR002018; CarbesteraseB.
InterPro; IPR002018; Ser_estrs_site.
InterPro; IPR000379; Ser_estrs_site.
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SEQUENCE
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al Similarity 46.0%;
262; Conservativo
                                                                                                                                                                                                              GILMSGNAICPWANTQCQHRAFTLAKLAGYKGEDNDKDVLEFLMKAKPQDLIKLEEKVLT
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                                                                                    FYLFNCIPAWKLNKSSEEYRTIERMIGMWTAFAENSSPQCPE---LEPIQWEPL-DSNAT 530
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                                           AKCLNISQQLKFIKLPERKQLKVWDSFYEK
                                                               YKCLNISDELKMIDVPEMDKIKQWESMFEK 565
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2: /cgn2_6/ptodata/1/laa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/laa/6A_COMB.pep:*

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RESULT 2
US-08-669-524-3
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TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-669-524-3
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APPLICANT:
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                                                                                  Query Match
Best Local Similarity
                                                                        Matches
                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 570 amino acids
                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Price, Robert L.
REGISTRATION NUMBER: 22,685
REGISTRATION NUMBER: 1451
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATE PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: OAKESHO
APPLICANT: SMYTH,
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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                                                                                                                                                                   TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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BOYCE, Thomas M.
CAMPELL, Peter M.
PARKER, Anthony G.
OAKESHOTT, John G.
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NEWCOMB, Richard D.
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pred. No. 1.1e-312;
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APPLICANT: Commonwealth Scientific and Industrial Rsrch. Org
TITLE OF INVENTION: MALATHION CARBOXYLESTERASE
FILE REFERENCE: Attorney Docket No. 6235515 50179-051
CURRENT APPLICATION NUMBER: US/09/068,980A
CURRENT FILING DATE: 1998-05-20
CARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER PILING DATE: 1996-11-23
EARLIER PILING DATE: 1995-11-23
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
FERRITE FILING DATE: 1995-11-23
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Best Local S
Matches 569
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TYPE: PRT
ORGANISM: Lucilia cuprina
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               LNPETKRPVLVYIHGGGFIIGENHRDMYGPDYFIKKDVVLINIQYRLGALGFLSLNSEDL 180
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                                                                IPYAQPPVGELRFKAPQRPTPWDGVRDCCNHKDKSVQVDFITGKVCGSEDCLYLSVYTNN 120
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                                                                                                                                                                Conservative
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Pred. No. 5.9e
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US-09-068-960-4
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US-09-068-960-4
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Best Local S
Matches 569
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
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Patent No. 6235515
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TITLE OF INVENTION: MALATHION CARBOXILESTERASE
FILE REFERENCE: Attorney Docket No. 6235515 50179-051
CURRENT APPLICATION NUMBER: US/09/068,960A
CURRENT FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER APPLICATION NUMBER: BCT/AU96/00746
EARLIER PILING DATE: 1996-11-22
EARLIER FILING DATE: 1995-11-23
EARLIER FILING DATE: 1995-11-23
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69; Conservative
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TITLE OF INVENTION: MALATHION CARBOXYLESTERASE
FILE REFERENCE: Attorney Docket No. 623515 50179
CURRENT APPLICATION UNMBER: US/09/068,960A
CURRENT FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER FILING DATE: 1996-11-22
EARLIER FILING DATE: 1996-11-23
EARLIER APPLICATION NUMBER: AU 6751
EARLIER OF SEO ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
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LENGTH: 570
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ORGANISM: Lucilia
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Pred. No. 5.9e-312;
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patent No. 6235515
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LENGTH: 570
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EARLIER APPLICATION NUMBER: US/09/068,960A
CURRENT FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER FILING DATE: 1996-11-22
EARLIER FILING DATE: 1995-11-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: MALATHION CARBOXYLESTERASE FILE REFERENCE: Attorney Docket No. 6235515 50
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                    QMPMLVKELETCVNEVPSELADAERTAPETLEMGAKIKKAHVTGETPTADNEMDLCSHIY 420
                                                            EERTNKVMFPFGPTVEPYQTADCVLPKHPREMVKTAWGNSIPTMMGNTSYEGLFFTSILK
                                                                         EERTNKVMFDFGPTVEPYQTADCVLDKHPREMVKTAWGNSIPTMMGNTSYEGLFFTSILK 360
FWFPMHRLLQLRENHTSGTPVYLYRFDFDSEDLINPYRIMRSGRGVKGYSHADELTYFFW
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                                                                                                                                                                                                                                                                                                                      Score 3060; DB 4;
Pred. No. 5.9e-312;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                            Length 570;
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                                                                                                                          Best Local Similarity Matches 563; Conserv
                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0. CURRENT APPLICATION NAMBER: US/08/669,5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Price, ROBERT L.
REGISTRATION NUMBER: 22,685
REFERENCE/DOCKET NUMBER: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
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            121
                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                       TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sir
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                                   61
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                                                                              NQLAKRMPKESRBYKTIERMTGIMIQFATTGNPYSNEIEGMENVSWDPIKKSDEVYKCLN
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, Application US/08669524 5843758
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                                                                                                                                                                                       TYPE:
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99 Canal Center Plaza, Suite 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMYTH, Kerrie A.
VENTION: ENZYME BASED BIOREMEDIATION
                                                                                                                                                                                                                                     570 amino acids
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NEWCOMB, Richard D.
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                                                                                                                              Conservative
                                                                                                                                                                                                   linear
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                                                                                                                                                                                      peptide
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                                                                                                                                          98.9<del>8</del>;
98.8<del>8</del>;
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                                                                                                                              Score 3040; D
Pred. No. 7.4e
2; Mismatches
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7.4e-310;
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; LENGTH: 570
; TYPE: PRT
; ORGANISM: Musca domestica
US-09-068-960-13
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US-09-068-960-13
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                                                                                                                                                                                                                                                                                            Matches
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TITLE OF INVENTION: MALATHION CARBOXYLESTERASE
FILE REFERENCE: Attorney Docket No. 623515 50179-051
CURRENT APPLICATION NUMBER: US/09/068,960A
CURRENT FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER FILING DATE: 1996-11-22
EARLIER FILING DATE: 1996-11-22
EARLIER FILING DATE: 1995-11-23
NUMBER: OF SEQ. ID NOS: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver.
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423; Conservation
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                 NVPGNAGLKDQVMALRWVKSNIAIFGGDVDNITVFGESAGGASTHYMMITEQTRGLFHRG
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                                                                                    LNPDKRRPVMVFIHGGDFIFGEANRNWFGPDYFMKKPVVLVTVQYRLGVLGFLSLKSENL
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                                                                                                                                                                                                                                                                                     73;
                                                                                                                                                                                                                                                                                        Score 2348; DB 4;
Pred. No. 2.9e-237;
73; Mismatches 74;
                                                                                                                                                                                                                                                                                                                      Length 570;
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Query Match
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64.98;

Score 1994.5;

DB 2

Length 572;

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US-08-669-524-8
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                                                                                                                         TELEFAX: 703-684-1124 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Price, Robert L.
REGISTRATION NUMBER: 22,685
               MOLECULE TYPE:
                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 572 amino acids
                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 703-684-1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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STATE: Virginia
COUNTRY: USA
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                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE:
                                                                         TYPE:
                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
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99 Canal Center Plaza, Suite 300
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BOYCE, Thomas M.
CAMPELL, Peter M.
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NEWCOMB, Richard D.
                                                                                                                                                                                                                                                                                                                                                             IBM PC compatible SYSTEM: PC-DOS/MS-DOS
                                   linear
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Local Similarity

63.9%;

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: COMMONWEALTH Scientific and Industrial Rsrch. Org
APPLICANT: COMMONWEALTH SCIENTIFIC AND INVESTIGASE
FILE REFERENCE: Attorney Docket No. 6235515 50179-051
FILE REFERENCE: Attorney Docket No. 6235515 50179-051
CURRENT APPLICATION NUMBER: US/09/068,960A
CURRENT FILING DATE: 1998-05-20
EARLIER APPLICATION NUMBER: PCT/AU96/00746
EARLIER APPLICATION NUMBER: AU 6751
EARLIER APPLICATION NUMBER: AU 6751
EARLIER FILING DATE: 1995-11-23
RARLIER FILING DATE: 1995-11-23
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                                                                                                                                           US-09-068-960-43
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                                                                                      Query Match
Best Local Similarity
                                                                     Matches
                                                                                                                                                            TYPE: PRT
ORGANISM: Lucilia cuprina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MNKNLGEVERLRKRIKTIEHKVQQYRQSTNETVVADTEYGQVRGIKRLSLYDVPYESFEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WNOLAKRMPKESREYKTIERMTGIWIQFATTGNPYSNEIEGMENVSWDPIKKSDEŸYKCL 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLMPQVLQQLDAGTPFIPKELLATEPSKEKLDSWSAQIRDVHRTGSESTPDNYMDLCSIY 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KOMPMLVKELETCVNFVPSELADAERTAPETLEMGAKIKKAHVTGETPTADNFMDLCSHI 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YEWEPMHRLLQLRENHTSGTPVYLYREDEDSEDLINPYRIMRSGRGVKGVSHADELTYFF
QVDFITGKVCGSEDCLYLSVYTNNLNPETKRPVLVYIHGGGFIIGENHRDMYGPDYFIKK 156
                                                                       206;
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                                                                                        35.4%;
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11; Mismatches 114;
                                                                           0;
                                                                           Score 1089; DB 4;
Pred. No. 6.2e-106;
0; Mismatches 1;
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                                                                                                                  Length 207;
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US-08-747-221B-37
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                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08,
FILING DATE: NO. 6663610en
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkir
REGISTRATION NUMBER: 37,4
                                                                                                                                                                                                                                                                                                                                           TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESSE: CAROL Talkington Verser,
ADDRESSEE: Heska Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Silver, Gary W. APPLICANT: Wisnewski, Nancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordberfect for Windows, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NO. 6063610el Carboxylesterase Nucleic TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181
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                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 37,459
REGISTRATION NUMBER: FC
REFERENCE/DOCKET NUMBER: FC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1825 Sharp Point Drive CITY: Fort Collins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
    220
                               131
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                                                                                                                                                                     40 GKVKGVKRLTVYDDSYYSFEGIPYAQPPVGELREKAPQRPTPWDGVRDCCNHKDKSVQVD 99
                                                                                                                                                                                                  Local Similarity
nes 193; Conserv
                                                                                    71
                                                                                                                                          11 GTLKGKEQISEKGNVFHSYSGIPYAKPPVGDLRFKPPQPAEPWSGVLDASKEGNSCRSVH 70
                                                                                                                                                                                                                                                                                                                LENGTH:
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                                                                                   GAASTHYMMLTEOTRGLFHRGILMSGNAICPWANTQCQH-----RAFTLAKLAGYKGEDN 274
                               LINIQYRLGALGELSLNSEDLNVPGNAGLKDQVMALRWIKNNCANEGGNPDNITVEGESA 219
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                                                                                                                                                                                                                                                                                                amino acid
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                                                                                                                                                                                                                                                                                                                                                          970/484-9505
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                                                                                                                                                                                                    Conservative 106; Mismatches
                                                                                                                                                                                                                                                                                         linear
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6063610ember 12,
                                                                                                                                                                                                                   27.9%;
                                                                                                                                                                                                                                                                                                                                                 37:
                                                                                                                                                                                                                                                                                                                                                                                                                                 lkington
                                                                                                                                                                                                           Score 856; DB 3;
pred. No. 8.3e-81;
l6; Mismatches 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1996
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                                                                                                                                                                                                                                      Length 528;
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RESULT 12
US-09-005-051-37
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; MOLECULE TYPE: US-09-005-051-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 37, Application US/09005051
Patent No. 6591222
GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Wisnewski, Nancy
                                                                                                                 TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: Windows 95 SOTTWARE: WordPerfect for Windows, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                        TELEPHONE: 970/493-7272
                                                                                                                                                                                                                                                 PRIOR APPLICATION UDMBER: 08/747,221
APPLICATION NUMBER: 08/747,221
FILING DATE: NO. 6291222ember 12,
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: (CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     441 VYLYRFDFD----SEDLINPYRIMRSGRGVKGVSHADELTYFF---WNQLAKRMPKESR 492
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                                      TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                           REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
                                                                                                                                                                                                               NAME: Verser, Carol Talkington REGISTRATION NUMBER: 37,459
                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Carol Talkington Verser,
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
                                                                         LENGTH:
                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EYKTIERMTGIWIQFATTGNPYSNEIEGMENVSWDPIKKSDEVYKCLNISDELKMIDVPE
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                                                                                                                                          SEQ ID NO 15
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Best Local Similarity
                          Best
                                                                                                                                                                                                                                                                                                                                                                Sequence 15, Application US/09068960A Patent No. 6235515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 193;
        Matches 153;
                                                                                                                                                      EARLIER FILING DATE: 1996-11-22
EARLIER APPLICATION NUMBER: AU 6751
EARLIER FILING DATE: 1995-11-23
NUMBER OF SEQ 1D NOS: 43
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/068,960A CURRENT FILING DATE: 1998-05-20 EARLIER APPLICATION NUMBER: PCT/AU96/00746
                                                                                                                                                                                                                                                                           TITLE OF INVENTION: MALATHION CARBOXYLESTERASE FILE REFERENCE: Attorney Docket No. 6235515 50179-051 CURRENT APPLICATION NUMBER: US/09/068,960A
                                                                                                                                                                                                                                                                                                                               APPLICANT: Commonwealth Scientific and Industrial Rsrch.
                                                                                     TYPE: PRT
ORGANISM: Musca domestica
                                                                                                                        LENGTH: 207
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                        Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVVNRERLLQLWINFAKIGNP-TPEINDVITTKWD--KATEEKSDHMDIDNTLRMIPDPD
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       Similarity 74.6
53; Conservative
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Pred. No. 8.3e-81;
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                                                                                                                                                                                                  Best Local Similarity
Matches 182; Conserv
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INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 530 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
OPERATING SYSTEM: Windows, Version
SOFTWARE: WordPerfect for Windows, Version
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/747,221B
APPLICATION UNBER: US/08/747,221B
FILING DATE: No. 6063610ember 12, 1996
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Silver, Ga
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                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
                                                                                      115 SVYTNNLNPETKRPVLVYIHGGGFIIGENHRDMYGPDYFIKKDVVLINIQYRLGALGFLS 174
                                                                                                                                                                                                                                                                                                           TYPE: amino acids
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DILEFLMKANPYDLIKEEPQVLTPE 205
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                                                                                                                                   YFSYTGVPYAKPPVGELREKPPOKAEPWNGVFNATSHGNVCKALNEFLKKIEGDEDCLLV
                                                                                                                                                                  YYSFEGIPYAQPPYGELREKAPORPTPWDGVRDCCNHKDKSVQVDFITGKVCGSEDCLYL 114
                            LNSEDLNVPGNAGLKDQVMALRWIKNNCANFGGNPDNITVFGESAGAASTHYMMLTEQTR 234
                                                                  NVYAPKTTSDKKLPVFFWVHGGGFVTGSGNLEFQSPDYLVNYDVIFVTFNYRLGPLGFLN 144
LELE--GAPGNVGLLDQVAALKWTKENIEKFGGDPENITIGGVSAGGASVHYLLLSHTTT 202
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                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                           87; Mismatches
                                                                                                                                                                                                                           Score 785.5; DB 3;
Pred. No. 2.1e-73;
                                                                                                                                                                                                                                                   Length 530;
                                                                                                                                                                                                                  Indels
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                                                                    US-09-005-051-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
Query Match 25.6 Best Local Similarity 34.3 Matches 182; Conservative
                                                                                                                                        TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE S30 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    203 GLYKRAIAQSGSALNEWAFQRHPVKRSLQLAEILGHP-TNNTQDALEFLQKAPVDSLLKK
                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Silver, Ga. APPLICANT: Wisnewski,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  262 MPAETEGEIIEE-----FVFVPSIEK-----VFPSHQPFLEESPLARMKSGSFNKVPL 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     235 GLEHRGILMSGNAICPWA-NTQCQHRAFTLAKLAGYKGEDNDKDVLEFLMKAKPQDLIK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       511 GNPYSNEIEGMENVSWDPIKKSDEVYKCLNISDELKMIDVPEMDKIKQWE 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360 AEKIRKFYF-DDKPVPENEOKFIDLIGDIWFTRGIDKHVKLSV-EKODEPVYYYEYSFSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               394
                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
CRASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 08/747,221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/747,221
FILING DATE: No. 6391222ember 12,
ATTORNEY/ACENT INFORMATION:
                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Carol Talkington Verser, Ph.D. ADDRESSEE: Heska Corporation STREET: 1825 Sharp Point Drive CITY: Fort Collins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: FC-
                                                                                                                                                                                                                                                               NAME: Verser, Carol Talkington REGISTRATION NUMBER: 37,459
                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVGFNSAEGLLYKFFNKEKPEMLNQAE-----ADFERLVPAEFELAHGSEESKKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MMGNTSYEGLFFTSILKOMPMLVKELETCVNFVPSELADAERTAP-----ETLEM 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --LEEKVLTLBERTNKVMFPFGPTVEPYQTADCVLPKH-----PREMVKTAWGNSIPT 343
                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GNP-TPEVTELLPVKWEPATKDKLNY--LNIDATLTLGTNPEETRVKFWE 521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDLINPYRIMRSGRGVKGVSHADELTYFFWNQLAKRMPKESREYKTIERMTGIWIQFATT
                                                                                                                        amino acid
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                                                                                                                                              530 amino acids
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No. 6291222el Carboxylesterase Nucleic
Molecules, Proteins and Uses Thereof
                        25.6%;
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         Score 785.5; DB 4
Pred. No. 2.1e-73;
7; Mismatches 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                Version 7.0
                                                 DB 4;
                                                 Length 530;
                  Indels
                      57;
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                      511 GNPYSNEIEGMENVSWDPIKKSDEVYKCLNISDELKMIDVPEMDKIKQWE 560
                                                418 S---HPAKGTFGDHNLTGACHGEELVNLFKVEMMKLEKDKPNVLLTKDRVLAMWTNFIKN 474
                                                                      451 EDLINPYRIMRSGRGVKGVSHADELTYFFWNQLAKRMPKESREYKTIERMTGIWIQFATT 510
                                                                                                                394 GAKIKKAHVTGETPTADN---FMDLCSHIYFWFPMHRLLQLRFNHTSGTDVYLYRFDFDS 450
                                                                                                                                                  310 LVGFNSAEGLLYKFFMKEKPEMLNQAE------ADFERLVPAEFELAHGSEESKKL 359
                                                                                                                                                                    262 MPAETEGEIIEE-----FVFVPSIEK-----VFPSHQPFLEESPLARMKSGSFNKVPL 309
                                                                                                                                                                                                                       293 --LEEKVLTLEERTNKVMFPFGPTVEPYQTADCVLPKH------PREMVKTAWGNSIPT 343
                                                                                                                                                                                                                                                                                                                                                          360 AEKIRKFYF-DDKPVPENEQKEIDLIGDIWFTRGIDKHYKLSV-EKQDEPVYYYEYSFSE 417
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Search completed: April 4, 2003, 09:18:06 Job time : 17.7722 secs

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Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                 Database :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
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Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

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11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       April 4, 2003, 09:16:33; Search time 24.5753 Seconds (without alignments)
1417.991 Million cell updates/sec
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3073
1 MNFNVSLMEKLKWKIKCIEN.....PEMDKIKQWESMFEKHRDLF 570
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	718	23.4	574	9	US-10-023-515-4	Sequence 4, Appli
N	718	23.4	612	9	US-09-875-353-4	Sequence 4, Appli
ω	707.5	23.0	585	10	US-09-934-323-4	**
4	571.5	18.6	602	10	US-09-748-739A-2	•
ហ	565	18.4	574	10	US-09-748-739A-6	σ,
o,	564	18.4	574	10	US-09-748-739A-8	Sequence 8, Appli
7	563	18.3	574	10	US-09-748-739A-17	17
80	563	18.3	574	10	US-09-748-739A-20	20
9	561	18.3	574	10	US-09-748-739A-4	Sequence 4, Appli
10	558	18.2	574	10	US-09-748-739A-19	Sequence 19, Appl
11	558	18.2	574	10	US-09-748-739A-21	Sequence 21, Appl
12	556	18.1	574	10	US-09-748-739A-18	Sequence 18, Appl
13	554	18.0	574	10	US-09-748-739A-22	
14	548	17.8	537	9	US-09-738-626-4754	Sequence 4754, Ap
15	526	17.1	574	10	US-09-748-739A-23	Sequence 23, Appl
16	525.5	17.1	581	9	US-10-023-515-2	Sequence 2, Appli
17	522	17.0	549	9	US-10-102-806-689	Sequence 689, App
18	507.5	16.5	565	10	US-09-895-860-5	Sequence 5, Appli
19	495.5	16.1	554	10	US-09-895-860-4	Sequence 4, Appli

#### ALIGNMENTS

	Db 121 GFMFGSGHSLPLSLYDGESLAREGNVIVVSINYRLGPLGFLSTGDDKLPGSGNYGLLDQR 180
	QY 137 GFIIGENHRDMYGPDYFIKK-DVVLINIQYRLGALGFLSLNSEDLNVPGNAGLKDQV 192
	Qy 98 VDFITGKVCGSEDCLYLSVYT-NNLNPETKRPVLVYIHGG 136
	Qy 40 GKVKGVKRLTVY-DDSYYSFEGIPYAQPPVGELRFKAPQ-RPTPWDGVRDCCNHKDKSVQ 97
18;	Query Match 23.4%; Score 718; DB 9; Length 574; Best Local Similarity 33.6%; Pred. No. 1.1e-57; Matches 187; Conservative 83; Mismatches 223; Indels 64; Gaps
	; FEATURE: ; OTHER INFORMATION: Consensus sequence US-10-023-515-4
	TYPE: PRT ORGANISM: Artificial Sequence
	; SEQ ID NO 4 ; LENGTH: 574
	; NOMBER OF SEQ 1D NOS: 0 ; SOFTWARE: FastSEQ for Windows Version 4.0
	PRIOR FILING DATE: 2001-03-28
	; PRIOR FILING DATE: 2000-12-18; PRIOR APPLICATION NUMBER: 60/279,508
	PRIOR APPLICATION NUMBER: 60/256,369
	; CURRENT ETLING DATE: 2001-12-18
	; FILE REFERENCE: 10448-122001
	; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
	; APPLICANT: Curtis, Rory A. J. ; APPLICANT: Silos-Santiago, Inmaculada . minis of INVENTATION 52010 A NOVEM HINAN CARROLUS
	; Publication No. US20020182636A1 ; GENERAL INFORMATION:
	RESULT 1 US-10-023-515-4 ; Sequence 4, Application US/10023515

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181

LALKWVQDNIAAFGGDPNSVTIFGESAGAASVSLLLLSNGGDNPPSSKGLFHRAISQSGS

MALRWIKNNCANFGGNPDNITVFGESAGAASTHYMMLTE-----OTRGLFHRGILMSGN 246

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Sequence 4, Application US/09875353

Patent No. US20020168713A1

Patent No. US20020168713A1

Patent No. US20020168713A1

Patent No. US20020168713A1

Patent No. US20020168713A1

PATENT OF INVENTION: 46980, A NOVEL HUMAN NEUROLIGIN FAMILY

PATENT OF INVENTION: MEMBER AND USES THEREOF

PATENT REFERENCE: 10448-058001

CURRENT FILING DATE: 2001-06-06

PRIOR APPLICATION NUMBER: US 60/209,949

PRIOR APPLICATION NUMBER: US 60/209,949

PRIOR FILING DATE: 2000-06-06

NUMBER OF SEQ ID NOS: 6

SOPTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4

LENGTH: 612
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US-09-875-353-4
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Best Local Similarity
Matches 187; Conserv
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   247
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                                                                                                                                                                                                                                                                                           40 GKVKGVKRLTVY-DDSYYSFEGIPYAQPPVGELRPKAPQ-RPTPWDGVRDCCNHKDKSVQ 97
                                                                                                                                                                                                                                 98 VDFI----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALSPWAIQSESNARGRAKELARLLGC-NETSSSELLDCLRSKSAEELLEATRSFLLFEYV 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPTADNEMBLCSHIYEWEPMHRLLQLRENHTSGTPVYLYREDEDSEDLINPYRIMRSGRG 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFLPLFLAFGPVVDGDDAPEAFIPEDPEELIKEGKFADVPYLIGVTKDEGGYFAAMLLNA 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KP---NLQDMLTDLLFKCPTRVAADLHAKH-GGSPVYAYVFDHPASFGIGQFLAKRVDPE 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSKGEDELKKETNPDVWLELLKYLLFYASEALNIKDMDDLADKVLEKYPGDVDDFSVESR 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----KQMPMLVKELETCVNFVPSE---LADAERTAPETLE-MGAKIKKAHVTGE 405
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                                                                                                                                                 GFIIGENHR---DMYGPDYFIKK-DVVLINIQYRLGALGFLSLNSEDLNVPGNAGLKDQV 192
                                                                                                                                                                                         DDDFGFSLSDLKVALKMLSLGWNKLVGLKLSEDCLYLNVYTPKNTKPNSKLPVMVWIHGG
                                                                                                                                                                                                                                                                     MALRWIKNNCANFGGNPDNITVFGESAGAASTHYMMLTE-----QTRGLFHRGILMSGN
                                                                                                                   GFMFGSGHSLPLSLYDGESLAREGNVIVVSINYRLGPLGFLSTGDDKLPGSGNYGLLDQR
 AICPWA---NTQCQHRAFTLAKLAGYKGEDNDKDVLEFLMKAKPQDLIKLEEKVLTLEER
                                         LALKWYQDNIAAFGGDPNSYTIFGESAGAASYSLLLLSNGGDNPPSSKGLFHRAISQSGS
                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                consensus sequence
                                                                                                                                                                                                                 -----TGKVCG---SEDCLYLSVYT-NNLNPETKRPVLVYIHGG
                                                                                                                                                                                                                                                                                                                                                                    23.4%;
                                                                                                                                                                                                                                                                                                                                                 ; Score 718; DB 9; ; pred. No. 1.3e-57; 83; Mismatches 223;
                                                                                                                                                                                                                                                                                                                                                                                        Length 612;
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US-09-934-323-4
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; OTHER INFORMATION: Consensus sequence
US-09-934-323-4
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APPLICANT: Curtis, Rory A. J.

TITLE OF INVENTION: 33410, A NOVEL HUMAN CARBOXYLESTERASE

TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF

FILE REFERENCE: 10448-081001

CURRENT FILING LOTE: 2001-08-21

PRIOR APPLICATION NUMBER: US 60/226,774

PRIOR APPLICATION NUMBER: US 60/226,774

PRIOR FILING DATE: 2000-08-21

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 585
TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                            VMALRWIKNNCANFGGNPDNITVFGESAGAASTHYMMLTE-----QTRGLFHRGILMSG
                                                                                                                                                                              GKVRGVNEKTDNGEQSVYSFLGIPYAEPPVGNLRFKAPQPYKEPWSDVLDATKYPPSCLQ 70
                                                                                                                                                                                                                                                                                                                            GKVKGVKRLTVY-DDSYYSFEGIPYAQPPVGELRFKAPQ-RPTPWDGVRDCCNHKDKSVQ 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NVSWDPIKKSDEVYKCL
                                                                GFIIGENHR---DMYGPDYFIKK-DVVLINIQYRLGALGFLSLNSEDLNVPGNAG-LKDQ 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -VVWPKYTSEEQKYSLL
SALSPWAIQSESNARGRAKELARLLGC-NETSSSELLDCLRSKSAEELLEATRSFLLFEY
                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                             23.0%; Score 707.5; DB 10; 33.5%; Pred. No. 1.1e-56; tive .83; Mismatches 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              539
                                                                                                                                                                                                                                                                                ----TGKVCG---SEDCLYLSVYT-NNLNPETKRPVLVYIHGG 136
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RESULT 4
US-09-748-739A-2
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US-09-748-739A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 18.6%; Score 571.5; DB 10; Length 602; Best Local Similarity 29.0%; Pred. No. 4e-44; Matches 176; Conservative 97; Mismatches 227; Indels 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lockridge, Oksana
APPLICANT: Watkins, Jeffry D.
APPLICANT: Watkins, Jeffry D.
TITLE OF INVENTION: Butrylcholinesterase Variants and
TITLE OF INVENTION: Methods of Use
TILE REFERENCE: P-IX 4143
CURRENT APPLICATION NUMBER: US/09/748,739A
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                    222
341 KKTQILVGVNKDEGTWF--LVYGAPGFSKDNNSII--TRKEFQEGLKIFFPGVSEFGKES 396
                                                                                                                                                             230
                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 KWKIKCIENKFLNYRLT-----TNETVVAETEYGKVKGVKRLTVYDDSYYSFEGIP 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 KVTIICI--RFLFWFLLLCMLIGKSHTEDDIIIATKNGKVRGM-NLTVFGGTVTAFLGIP 60
                                                                                                                                                                                                                                                                                                                                               VCGSEDCLYLSVYTNNLNPETKRPVLVYIHGGGFIIGENHRDMYGPDYFIKKD-VVLINI 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENVSWDPIKKSDEVYKCL 539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RKP---NLQDMLTDLLFKCPTRVAADLHAKH-GGSPVYAYVFDHPASFGIGQFLAKRVDP 485
                                     NSIPTMMGNTSYEGLFFTSILKQMPMLVKELETCVNFVPSELADAERT-APETLEMGAKI 397
                                                                                                                     LEFLMKAKPODLIKLEEKVLTLEERTNKVMFPFGPTVEPYOTADCVLPKHPREMVKTAWG
                                                                                                                                                                                                                                                                                                                        ---SEDCLYLNVWIPAPKPK-NATVLIWIYGGGFQTGTSSLHVYDGKFLARVERVIVVSM 172
                                                                                                                                                                                                                                                                                                                                                                                                   YAQPPLGRLRFKKPQSLTKWSDIWNATKYANSCCQNIDQSFPGFHGSEMWNPNTDL----
                                                                                                                                                                                                                                                                                                                                                                                                                            YAQPPVGELREKAPQRPTPWDGV------RDCCNHKDKSV------QVDFTTGK 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EFGGAVHGDEIFFVFGNPLLKEQLYKATEEEEKSSSKTMMNYWANFAKTGNPNNGTSNGL 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ETPTADNFMDLCSHIYFWFPMHRLLQLRFNHTSGTPVYLYRFDFDSEDLINPYRIMRSGR 464
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                                                                                                                                                           ASVSLHLLSPGSHSLFTRAILOSGSFNAPWAVTSLYEARNRTLNLAKLTGCSRE-NETEI 288
                                                                                                                                                                                                ASTHYMMLTEQTRGLFHRGILMSGNAICPWANT---QCQHRAFTLAKLAGYKGEDNDKDV 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --VVWPKYTSEEQKYSLL 561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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	-LCSHIYEWFPMHRLLQLRENHTSGTPVYLIYREDEDSEDLINPYRIMRSGRGV 466	415 -	Qy	
	NNSIITRKEFQEGLKIFFPGVSEFGKESILFHYTDWV	339 1	Db	
	KELETCVNFVPSELADAERT-APETLEMGAKIKKAHVTGETPTADNFMD 414	367 1	Qy	
	LSVNEGPTVDGDFLTDMPDILLELGQFKKTQILVGVNKDEGTAFLVYGAPGFS 338	286 1	Дb	
	VMFPFGPTVEPYQTADCVLPKHPREMVKTAWGNSIPTMMGNTSYEGLFFTSILKQMPMLV 366	307 1	Qy	
	PWAVTSLYEARNRTLNLAKLTGCSRE-NETELIKCLRNKDPQEILLNEAFVVPYGTQ 285	230 1	DЪ	
	PWANTQCQHRAFTLAKLAGYKGEDNDKDVLEFLMKAKPQDLIKLEEKVLTLEERTNK 306	250 1	Qy	
	DQQLALQWVQKNIAAFGGNPKSVTLFGESAGAASVSLHLLSPGSHSLFTRAILQSGSFNA 229	170 1	Db	
	DQVMALRWIKNNCANFGGNPDNITVFGESAGAASTHYMMLTEQTRGLFHRGILMSGNAIC 249	190 [	Qy	
	IYGGGFQTGTSSLHVYDGKFLARVERVIVVSMNYRVGALGFLALPGNPEAPGNMGLF 169	113	Db	
	AVN d	133	Qy	
	YANSCCQNIDQSFPGFHGSEMWNPNTDLSEDCLYLNVWIPAPKPK-NATVLIW 112	61 1	: Db	
	SVQVDFITGKVCG	86 -	Qy	
	DDIIIATKNGKVRGM-NLTVFGGTVTAFLGIPYAQPPLGRLRFKKPQSLTKWSDIWNATK 60	2 1	Db	
	TVVAETEYGKVKGVKRLTVYDDSYYSFEGIPYAQPPVGELRFKAPQRPTPWDGV 85	31 1	Qy	
23;	Match 18.4%; Score 565; DB 10; Length 574; Local Similarity 29.0%; Pred. No. 1.5e-43; les 168; Conservative 95; Mismatches 220; Indels 96; Gaps 2	Query Mat Best Loca Matches	Qu Ma	
	OTHER INFORMATION: Human Butyrylcholinesterase variant 09-748-739A-6	OTHER 19-748-7	US-0	
	R: Artificial Sequence	ORGANISM:		
	DP 74 .	TYPE D		
	:: FastSEQ for Windows Version 4.0	OFTWARI		
		JRRENT	 <b>z</b> Q	
	ERENCE: P-IX 4143 APPLICATION NUMBER: US/09/748,739A	JRRENT	 Q *	
	TITLE OF INVENTION: BUTYPYICHOLINESTERASE VARIANTS AND TITLE OF INVENTION: Methods of Use	TILE OF	 1 +3 +3	
		PPLICAL	 A A	
	NFORMATION:	GENERAL I	GE	
	ULT 5 09-748-739A-6 Requence 6, Application US/09748739A Ratent No. US20020119489A1	SSULT 5 S-09-748-7 Sequence Patent No	S - S	
	WTSEPPK 556	550 ¥	Db	
	WESMFEK 565	559 V	Qy	
	SIVKRWANFAKYGNPNETQN-NSTSWPVFKSTEQKYLTLN-TESTRIMTKLRAQQCRF 549	494 9	Db	
	YSNEIEGMENVSWDPIKKSD	499 F	Qy	
	NAFFYYFEHRSSKLPWPEWMGVMHGYEIEFVFGLPLERRDNYTKAEEILSR 493	442 1	Db	
	RSGRGVKGVSHADELTYFFWNQLA	439 1	Qy	
	ILFHYTDWVDDQRPENYREALGDVVGDYNFICPALEFTKKFSEW	397 ]	Дb	
	KKAHVTGETPTADNFMDLCSHIYFWEPMHRLLQLRFNHTSG 438	398 1	Qy	

RESULT 8 US-09-748-739A-20

Application US/09748739A

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Patent No. US20020119489A1

Patent No. US20020119489A1

GENERAL INFORMATION:
APPLICANT: Lockridge, Oksana
APPLICANT: Matkins, Jeffry D.
APPLICANT: Matkins, Jeffry D.
TITLE OF INVENTION: Butyrylcholinesterase Variants and
TITLE OF INVENTION: Methods of Use
TITLE OF INVENTION: Methods of Use
TILE REFERENCE: P-1X 4143

CURRENT APPLICATION NUMBER: US/09/748,739A

CURRENT FILING DATE: 2000-12-06
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ORGANISM: Artificial Sequence
FEATURE: OTHER INFORMATION: Human Butyrylcholinesterase variant
US-09-748-739A-8
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US-09-748-739A-8
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SOFTWARE: FASTSEQ for
SEQ ID NO 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PWANT---QCQHRAFTLAKLAGYKGEDNDKDVLEFLMKAKPQDLIKLEBKVLTLEERTNK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           168; Conservative
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                                                                                                                                                                                                                                                               PWAYTSLYEARNRTLNLAKLTGCSRE-NETEIIKCLRNKDPQEILLNEAFVVPY---GTS
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                                                                                                                                                                                                                                                                                                                                                                                                                         THGGGFTIGENHRDMYGPDYFIKKD-VVLINIQYRLGALGFLSL- NSEDLNVPGNAGLK 189
                                                                                               --LCSHIYF-----WFPMHRLLQLRFNHTSGTPVYLYRFDFDSEDLINPYRIMRSGRGV
                                                                                                                                                                                                                             VMFPFGPTVEPYQTADCVLPKHPREMVKTAWGNSIPTMMGNTSYEGLFFTSILKQMPMLV 366
                               KGVSHADELTYFFWNQLAKRMPKESREYKTIERMTGIWIQFATTGNPYSNEIEGMENVSW
                                                                 NETCPALEFTKKESEW-------GNNAFFYYFEHRSSKLPWPEWM------
                                                                                                                               KDNNSII--TRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDVVGDY
                                                                                                                                                                KELETCVNFVPSELADAERT-APETLEMGAKIKKAHVTG--ETPTADNFMD------
-GVMHGYEIEFVFGLPLERRDNYTKAEEILSRSIVKRWANFAKYGNP--NETQN-NSTSW
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; Pred. No. 1.8e-43;
94; Mismatches 221;
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RESULT 7
US-09-748-739A-17
; Sequence 17, Application US/09748739A
; Patent No. US20020119489A1
; Patent No. US200720119489A1
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CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 574
TYPE: PRT
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TITLE OF INVENTION: Butyrylcholinesterase Variants
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: P-IX 4143
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PVFKSTEQKYLTLN-TESTRIMTKLRAQQCRFWTSFFPK 528
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                                 DPIKKSDEVYKCLNISDELKMIDVPEMDKIKQWESMFEK
                                                                  -GVMHGYEIEFVFGLPLERRDNYTKAEEILSRSIVKRWANFAKYGNP--NETQN-NSTSW 490
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68; Conservative
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-748-739A-20
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                                                                                                         Sequence 4, Application US/09748739A Patent No. US20020119489A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 168; Conserv
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LENGTH: 574
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APPLICANT: Watkins, Jeffry D.
TITLE OF INVENTION: Butyrylcholinesterase Variants
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: P-IX 4143
CURRENT APPLICATION NUMBER: US/09/748,739A
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
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             APPLICANT: Lockridge, Oksana
APPLICANT: Watkins, Jeffry D.
TITLE OF INVENTION: Butrylcholinesterase
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: P-IX 4143
CURRENT APPLICATION NUMBER: US/09/748,739A
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                                                                                                                                                                                                                                                                                                                 -GVMHGYEIEFVFGLPLERRDNYTKAEEILSRSIVKRWANFAKYGNP--NETQN-NSTSW
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29.0%;
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; Pred. No. 2.3e-43;
94; Mismatches 221
                                                      Variants
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RESULT 10
US-09-748-739A-19
, Sequence 19, Application US/09748739A
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; OTHER INFORMATION:
US-09-748-739A-4
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NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for W
SEQ ID NO 4
LENGTH: 574
Patent No. US20020119489A1

GENERAL INFORMATION:
APPLICANT: Lockridge, Oksana
APPLICANT: Watkins, Jeffry D.
TITLE OF INVENTION: Butyrylcholinesterase Variants
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: P-IX 4143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 168; Conserv
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TYPE: PRT
ORGANISM: Artificial
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                                                                                                                                                                                                    PVFKSTEQKYLTLN-TESTRIMTKLRAQQCRFWTSFFPK
                                                                                                                                                                                                                                     DPIKKSDEVYKCLNISDELKMIDVPEMDKIKQWESMFEK 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IHGGGFIIGENHRDMYGPDYFIKKD-VVLINIQYRLGALGFLSL--NSEDLNVPGNAGLK 189
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                                                                                                                                                                                                                                                                      -GVMHGYEIEFVFGLPLERRDNYTKAEEILSRSIVKRWANFAKYGNP--NETQN-NSTSW
                                                                                                                                                                                                                                                                                                                                                                                                     KDNNSII---TRKEFQEGLKIFFPGVSEFGKESILFHYTDWVDDQRPENYREALGDVVGDY
                                                                                                                                                                                                                                                                                                                                                                                                                                     KELETCVNFVPSELADAERT-APETLEMGAKIKKAHVTG--ETPTADNFMD------
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31
Windows Version
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Pred. No. 3.5e-43;
14; Mismatches 221;
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CURRENT APPLICATION NUMBER: US/09/748,739A
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19
LENCTH: \$74
TYPE: PRT

and

; ORGANISM: Homo sapiens US-09-748-739A-19

Query Match 18.2%; Score 558; DB 10; Best Local Similarity 29.0%; Pred. No. 6.5e-43; Matches 168; Conservative 93; Mismatches 222;

Length 574;.
Indels 9

Gaps

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US-09-748-739A-21
; Sequence 21, Application US/09748739A
; Patent NO. US20020119489A1
; GENERAL INFORMATION:
; APPLICANT: Lockridge, Oksana
; APPLICANT: Watkins, Jeffry D.
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; ORGANISM: Equus
US-09-748-739A-21
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CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 574
                                    Matches 167;
                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                           TITLE OF INVENTION: Butyrylcholinesterase Variants
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: P-IX 4143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      491 PVFKSTVQKYLTLN-TESTRIMTKLRAQQCRFWTSFFPK 528
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 ETVVAETEYGKVKGVKRLTVYDDSYYSFEGIPYAQPPVGELRFKAPQRPTPWDGV-----
                                      Conservative 100;
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                                    18.2%; score 558; DB 10; 29.2%; Pred. No. 6.5e-43; tive 100; Mismatches 232;
                                                                         Length 574;
                                           Indels
                                           72;
                                             Gaps
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              85
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	Watkins, C. NVENTION: BU NVENTION: IN ENCE: P-IX	APPLIC TITLE TITLE	
	Patent No. US20020119489A1 GENERAL INFORMATION: ADDITCANT: Lockridge, Oksana		
•	RESULT 12 US-09-748-739A-18 ; Sequence 18, Application US/09748739A	RESULT 1 US-09-74 ; Sequen	
	ĽN-	Db 503	
	9 LNISDELKMIDVPEMDKIKQMESMFEKHRDL 569	Оу 539	
502	LPLERRVNYTRAEEILSRSIMKRWANFAKYGNPNGTQNNSTRWPVFKSTEQKYLT	Db 448	
538	NQLAKRMPKESREYKTIERMTGIWIQFATTGNPYSNEIEGMENVSWDPIKKSDEVYKC	Qy 481	
447	FTRKFSELGNDAFFYYFEHRSTKLPWPEWMGVMHGYEIEFVFG	Db 405	
480	FWFPMHRLLQLRFNHTSGTPVYLYRFDFDSEDLINPYRIMRSGRGVKGVSHADELTYFFW	Qy 421	
404	-TRKEFQEGLKIFFPRVSEFGRESILFHYMDWLDDQRAENYREALDDVVGDYNIICPALE	Db 346	
420	FVPSELADAERT-APETLEMGAKIKKAHVTGETPTADNEMDLCSHIY	Qу 375	_
345	VDGDFLTDMPDTLLQLGQFKRTQILVGVNKDEGTAFLVYGAPGFSKDNNSII-	Db 294	_
374	VEPYQTADCVLPKHPREMVKTAWGNSIPTMMGNTSYEGLFFTSILKQMPMLVKELETCVN	Оу 315	_
293	EARNRTLTLAKRMGC-SRDNETEMIKCLRDKDPQEILLNEVFVVPYDTLLSVNFGPT	Db 238	_
314	QCQHRAFTLAKLAGYKGEDNDKDVLEFLMKAKPQDLIKLEEKVLTLEERTNKVMFPFGPT	Qy 255	~
237	VQKNIAAFGGNPRSVTLFGESAGAASVSLHLLSPRSQPLFTRAILQSGSSNAPWAVTSLY	Db 178	_
254	IKNNCANFGGNPDNITVFGESAGAASTHYMMLTBQTRGLFHRGILMSGNAICPWANT	Qy 198	_
177	QTGTSSLPVYDGKFLARVERVIVVSMNYRVGALGFLAL-SENPEAPGNMGLFDQQLALQW	Db 119	п
197	IIGENHRDMYGPDYFIKKD-VVLINIQYRLGALGFLSLNSEDLNVPGNAGLKDQVMALRW	Qy 139	2
118	YANSCYQNTDQSFP-GFLGSEMWNPNTELSEDCLYLNVWIPAPKPK-NATVMIWIYGGGF	Db 61	п
138	RDCCNHKDKSVQVDFITGKVCGSEDCLYLSVYTNNLNPETKRPVLVYIHGGGF	Оу 86	0
60	::  :  : :     : :          :      : :	Db 2	ь

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CURRENT APPLICATION NUMBER: US/09/748,739A
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 574
TYPE: PRT
ORGANISM: Homo sapiens
US-09-748-739A-18
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20
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Best Local Similarity
Matches 167; Conserv
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IHGGGFIIGENHRDMYGPDYFIKKD-VVLINIQYRLGALGFLSL--NSEDLNVPGNAGLK 189
                                                      --RDCCNHKDKSV------QVDFITGKVCGSEDCLYLSVYTNNLNPETKRPVLVY 132
                                                                                                 YANSCCQNIGQSFPGFHGSEMWNPNTDL-----SEDCLYLNVWIPAPKPK-NATVLIW 112
                                                                                                                                                                18.1%; Score 556; DB 10; Length 574; ilarity 28.8%; Pred. No. 1e-42; Conservative 94; Mismatches 222; Indels 9
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23;

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CURRENT APPLICATION NUMBER: US/09/748,739A
CURRENT FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 574
TYPE: PRT
ORGANISM: Felis catus
US-09-748-739A-22
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US-09-748-739A-22
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Patent No. US20020119489A1
GENERAL INFORMATION:
APPLICANT: Lockridge, Oksana
APPLICANT: Warkins, Jeffry D.
TITLE OF INVENTION: Butyrylcholinesterase Variants
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: P-1X 4143
                                                                                                                                                                                                                                                                                                                                                           Query Match 18.0%; Score 554; DB 10; Length 574; Best Local Similarity 28.1%; Pred. No. 1.5e-42; Matches 167; Conservative 100; Mismatches 201; Indels 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 491 PVFKSTEOKYLTLN-TESTRIMTKLRAQQCRFWTSFFPK 528
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                                                                            190 DQVMALRWIKNNCANFGGNPDNITVFGESAGAASTHYMMLTEQTRGLFHRGILMSGNAIC 249
                                                                                                                        113
                                                                                                                                           133 IHGGGFIIGENHRDMYGPDYFIKKD-VVLINIQYRLGALGFLSL--NSEDLNVPGNAGLK 189
                                                                                                                                                                                                                                                                                                     31 ETVVAETEYGKVKGVKRLTVYDDSYYSFEGIPYAQPPVGELRFKAPQRPTPWDGV-----
                                                                                                                                                                                                   61 YANSCYQNADQSFPGFPGSEMWNPNTDL-----SEDCLYLNVWIPTPKPK-NATVMIW 112
                                                                                                                                                                                                                                                                                      N
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PWA---NTQCQHRAFTLAKLAGYKGEDNDKDVLEFLMKAKPQDLIKLEEKVLTLEERTNK 306
                                       DQQLALQWVQKNIAAFGGNPKSVTLFGESAGAGSVSLHLLSPRSQPLFTRAILQSGSSNA 229
                                                                                                                                                                                                                                                                                  EDITITTKNGKVRGM-NLPVLDGTVTAFLGTPYAQPPLGRLRFKKPQFLTKWSDIWNATK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IYGGGFQTGTSSLPVYDGKFLARVERVIVVSMNYRVGALGFLALPGNPE---VPGNMGLF 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -GVMHGYEIEFVFGLPLERRDNYTKAEEILSRSIVKRWANFAKYGNP--NETQN-NSTSW 490
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	208 175	Qy 149 GPDYFIKKDVYLINIQYRLGALGFLSLNSEDLNVPGNAGLKDQVMALRWIKNNCANFGGN	
	148 115	Qy 91 HKDKSVQVDFI-TGKVCGSEDCLYLSVYTNNLNPETKRPVLVYIHGGGFIIG-ENHRDMY : :   :	
	90 57	Qy 31 ETVVAETEYGKVKGVKRLTVYDDSYYSFEGIPYAQPPVGELRFKAPQRPTPWDGVRDCCN : :	
22;	Gaps	Query Match 17.8%; Score 548; DB 9; Length 537; Best Local Similarity 29.2%; Pred. No. 4.9e-42; Matches 169; Conservative 97; Mismatches 220; Indels 92; Ga	
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		; SOFTWARE: PatentIn ver. 3.0 ; SEQ ID NO 4754 ; LENGTH: 537	
		PRIOR APPLICATION N PRIOR FILING DATE: NUMBER OF SEQ ID NO	
		PRI	
		PRIOR APPLICATION NUMBER: J	
		; FILE KEFEKENCE: 249-123; CURRENT APPLICATION NUMBER: US/09/738,626; CURRENT FILING DATE: 2000-12-18	
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		; APPLICANT: NAKAGAWA, SATOSHI ; APPLICANT: MIZOGUCHI, HIROSHI : APPLICANT- ANDO, SFIKO	
		Publication No. US20020197605A1 GENERAL INFORMATION:	
		ESULT 14 IS-09-738-626-4754 Sequence 4754, App	
		Db 481NGTQNNSTRWPAFRSTDQKYLTLN-AESPKYYTKLRAQQCRFWTLFFPK 528	
		QY 514 YSNEIEGMENVSWDPIKKSDEVYKCLNISDELKMIDVPEMDKIKQWESMFEK 565	
	480	435GVMHGYEIEFVFGLPLERRVNYTRAEEILSRSIMNYWANFAKYGNP	
	513	QY 454 INPYRIMRSGRGVKGVSHADELTYFFWNQLAKRMPKESREYKTIERMTGIWIQFATTGNP	
	434	:	
	453	QY 401 HVTGETPTADNEMDLCSHIYFWFPMHRLLQLRFNHTSGTPVYLYRFDFDSEDL	
	390	: ::       ::     ::     ::     ::     ::     ::     ::     ::     ::       ::     ::     ::     ::     ::     ::     ::     ::     ::     ::     ::     ::     ::     ::     ::     ::     ::     ::       ::       ::     ::     ::     ::     ::     ::     ::     ::     ::	
	400	67 KELETCVNKPPSELADAERTAPETLEMGAKIKKA	
	338	288 VNFGPVVDGDFLTDMPDTLLQLGQFKKTQILVGVNKDEGTAFLVYGAPGFS	
	366	307 VMFPFGPTVEPYQTADCVLPKHPREMVKTAWGNSIPTMMGNTSYEGLFFTSILKQMPMLV	
	287	Db 230 PWAVMSLDEAKNRTLTLAKFIGC-SKENDTEIIKCLRNKDPQEIL-LNELLVVPSDTLLS	

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NUMBER OF SEO ID NOS: 3.
SOFTWARE: FASTSEO for W.
SEO ID NO 23
LENGTH: 574
TYPE: PRT
ORGANISM: Rattus sp.
US-09-748-739A-23
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                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 161; Conserv
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APPLICANT: Watkins, Jeffry D.
TITLE OF INVENTION: Butyrylcholinesterase Variants
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: P-TX 4143
CURRENT APPLICATION NUMBER: US/09/748,739A
CURRENT FILING DATE: 2000-12-06
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                                                                                                                                                                                                                YANSCYONIDOAFPGFOGSEMWNPNTNLSEDCLYLNVWIPVPKPK-NATVMVWVYGGGFQ 119
                                                                                                                                                               IGENHRDMYGPDYFIKKD-VVLINIQYRLGALGFLSL--NSEDLNVPGNAGLKDQVMALR 196
                                                                                                                                                                                                                                               HKDKSVQ-VDFITGKVCG------SEDCLYLSVYTNNLNPETKRPVLVYIHGGGFI 139
                                                                                                                                                                                                                                                                                   EDVIITTKTGRVRGLS-MPILGGTVTAFLGIPYAQPPLGSLRFKKPQPLNKWPDVYNATK 60
TQCQHRAFTLAKLAGYKGEDNDKDVLEFLMKAKPQDLIKLEEKVLTLEERTNKVMFPFGP 313
                                                                    WIQRNIAAFGGNPKSVTLEGESAGAASVSLHLLCPQSYPLFTRAILESGSSNAPWAVKHP 236
                                                                                           WIKNNCANEGGNDDNITVEGESAGAASTHYMMLTEQTRGLEHRGILMSGNAICPWA---N 253
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31
Windows Version 4.0
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Search completed: April Job time: 27.5753 secs
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                                                                            497
                                                                                                                                            440 YEIEFVFGLPLERRVNYTRAEEIFSRSIMKTWANFAKYGHP--NGTQGNSTV-WPVFTST
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                                                                                                                                                                                                                                                                                                                          374 NEVPSELADAERTAPETLEM-----
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Title: Perfect score:

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Sequence:

OM nucleic - nucleic search, using sw model

GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

April 10, 2003, 22:59:47; Search time 2944.03 Seconds (without alignments) 16933.650 Million cell updates/sec

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result		% Query	:			•
NO.	Score	; ¬		DB	ID	Description
	1713	80.	1713		AR153442	R153442 Sequenc
	1711.4	99.9	1713		AR153439	153439 Sequenc
	1708.2	99.7	1713		AR153440	153440 Sec
	1703.4	99.4	1713		AR062837	062837 Sequenc
	1703.4	99.4	2240		AR153441 T.CII56636	153441 6636 Lu
	1678.2	98.0	1713		AR062838	AR062838 Sequence
, 0	987.2	57.6	2160		AF133341	133341
11	956.6	55.8	1710		AR153445	153445
12	678.8	39.6	2017		AY051473	051473 Drosophi
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	375.4	21.9 6	57335 57335		DMU51050	1050 Drosophila 015272 Drosophi
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سو،	370.6	6	$\sim$		AE003671	003671 Drosophi
20	363.8	21.2	1962		AY051497	051497 Drosophi
21	304.6	17.8	1906		AY058345	058345 Drosophi
22	300.4	17.5	13044		AC014297	014297 Drosophi
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25	300.4	17.5	$\sim$		AE003457	003457 Drosophi
26	288.2	16.8			AF216210	216210 Drosophi
28	270	150 150	1809		AF216215	210215
29	241.4	14.1	1630		CQESTA2EA	7988 C
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	Воус	9, T.M	χ.,	kes c	ott,J.Graham	Brownlie, J.Colin
TITLE	Mala	thion	carboxy	les	erase	

TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AR153442	VERRET
Robin,G.Charlesde.Quetteville., Claudianos,C., Smyth,KA., Boyce,T.Mark., Oakeshott,J.Graham. and Brownlie,J.Colin. Malathion carboxylesterase	Russell, R. Joyce., Newcomb, R. David., Campbell, P. Malcolm.,	1 (bases 1 to 1713)	Unclassified.	Unknown:	Unknown.		AR153442.1 GI:15120974	AR153442	Sequence 9 from patent US 6235515.	AR153442 1713 bp DNA linear PAT 08-AUG-20		

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Russell, R. Joyce., Newcomb, R. David., Campbell, P. Malcolm. Russell, R. Joyce., Newcomb, R. David., Claudianos, C., Smyth, K. Robin, G. Charlesde. Quetteville., Claudianos, C., Smyth, K. Boyce, T. Mark., Oakeshott, J. Graham. and Brownlie, J. Colin Boyce, T. Mark., Oakeshott, J. Graham. and Brownlie, J. Colin Malathion carboxylesterase Patent: US 6235515-A 1 22-MAY-2001;
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BASE CORIGIN	TITLE JOURNAI FEATURES SOUI	REFER AUT	KEYWORDS SOURCE ORGANI	ACCESSION VERSION	AR1534 LOCUS	B F CITT	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	дb	Qy	Дb	Qy	Db	Qy	Db	Qy	Db	Qy	Db
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:	Boyce, T.Mark., Oakesbott, J.Graham. and Brownlie, J.Col Malathion carboxylesterase Patent: US 6235515-A 3 22-MAY-2001; Location/Qualifiers 11713 e 11713	<pre>id., Campbell,P Claudianos,C.,</pre>	Jaknown. Unknown. Inclassified	AR153439 GI:15120971	AR153439		TCGATGTTTGAAAAACATAGAGATTTATTTTAG 1713	TCGATGTTTGAAAAACATAGAGATTTATTTTAG 1713	ATTAGTGATGAATTGAAAATGATTGATGTGCCTGAAATGGATAAGATTAAACAATGGGAG 1680	TTAGTGATGAATTGAAAATG	TGGGATCCAATTAAGAAATCCGATGAAGTATAC	GGAAAATGTTTCCTGGGATCCAATTAAGAAAT	TGGTATATGGATACAATTT	TGGTATATGGATACAATTTGCCACCACTGGTAATCCTTATAGCAATGAAATTGAAGG	AATCAATTGGCCAAACGTATGCCTAAAGAATCGCGTGAATACAAAACAATTGAACGTATG 1500	AATTGGCCAAACGTATGCCTAAAGAATCGCGTGAATACAAACAA	CGTAGTGGACGTGGTGTTAAGGGTGTTAGTCATGCTGATGAATTAACCTATTTCTTCTGG 1440	AGTGGACGTGGTGTTAAGGGTGTTAGTCATGCTGATGAATTAACCTATTTCTTCTG	GTCTACTTGTATCGCTTCGACTTCGATTCGGAAGATCTTATCAATCCCTATCGTATTATG 1380	TCGACTTCGATTCGGAAGATCTTATC	TICTGGTTCCCCATGCATCGTTGTTGCAATTACGTTTCAATCACACCTCCGGTACACCC 1320	TTCTGGTTCCCCATGCATCGTTTGTTGCAATTACGTTTCAATCACACCTCCGGTACACCC 1320	CATGTTACAGGAGAACACCAACAGCTGATAATTTATGGATCTTTGCTCTCACATCTAT 1260	GTTAC	GCTGATGTTGAACGCACCGCCCCAGAGACCCTTGGAAATGGGTGCTAAAATTAAAAAGGCT 1200	GATGCTGAACGCACCGCCCCAGAGACCTTGGGAAATGGGTGCTAAAATTAAAAAGG	CAAATGCCTATGCTTGTTAAGGAATTGGGAAACTTGTGTCAATTTTGTGCCAAGTGAATTG 1140	CAAATGCCTATGCTTAAGGAATTGGAAACTTGTGTGTCAATTTTTGTGCCAAGTGAATTG 1140	ATACCCACTATGATGGGTAACACTTCATATGAGGGTCTATTTTTCACTTCAATTCTTAAG 1080	CCACTATGATGGGTAACACTTCATATGAGGGTCTATTTTTCACTTCAATTCTTA	

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Russell,R.Joyce., Newcomb,R.David., Campbell,P.Malcolm., Russell,R.Joyce., Smyth,K.-A., Robin,G.Charlesde.Quetteville., Claudianos,C., Smyth,K.-A., Boyce,T.Mark., Oakeshott,J.Graham. and Brownlie,J.Colin. Boyce,T.Mark., Oakeshott,J.Graham. and Brownlie,J.Colin. Boyce,T.Mark., Oakeshott,J.Graham. and Brownlie,J.Colin. Boyce,T.Mark., Oakeshott,J.Graham. and Brownlie,J.Colin. Boyce,T.Mark., Oakeshott,J.Graham. and Brownlie,J.Colin. Boyce,T.Mark., Oakeshott,J.Graham. and Brownlie,J.Colin. Boyce,T.Mark., Oakeshott,J.Graham. and Brownlie,J.Colin. Boyce,T.Mark., Oakeshott,J.Graham. and Brownlie,J.Colin. Boyce,T.Mark., Oakeshott,J.Graham. and Brownlie,J.Colin. Boyce,T.Mark., Oakeshott,J.Graham. and Brownlie,J.Colin. Boyce,T.Mark., Oakeshott,J.Graham. and Brownlie,J.Colin. Boyce,T.Mark., Oakeshott,J.Graham. and Brownlie,J.Colin. Boyce,T.Mark., Oakeshott,J.Graham. and Brownlie,J.Colin. Boyce,T.Mark., Oakeshott,J.Graham. and Brownlie,J.Colin. Boyce,T.Mark., Oakeshott,J.Graham. and Brownlie,J.Colin. Boyce,T.Mark., Oakeshott,J.Graham. and Brownlie,J.Colin. Boyce,T.Mark., Oakeshott,J.Graham.
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Sequence 1
AR062837
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Unknown
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Patent: US 5843758-A 1 01-DEC-1998;
Location/Qualifiers
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Russell,R.Joyce., Newcomb,R.David.,
Boyce,T.Mark., Campbell,P.Malcolm.,
Oakeshott,J.Graham. and Smyth,K.-A.
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                                                                         GAAGAGCGTACAAATAAGGTCATGTTTCCTTTTGGTCCCACTGTTGAGCCATATCAGACCGAAGAGCGTACAAATAAGGTCATGTTTCCTTTTGGTCCCACTGTTGAGCCATATCAGACCGAAGAGCGTACAAATAAGGTCATGTTTCCTTTTGGTCCCACTGTTGAGCCATATCAGACC
                          ATACCCACTATGATGGGTAACACTTCATATGAGGGTCTATTTTTCACTTCAATTCTTAAG
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Russell,R.Joyce., Newcomb,R.David., Claudianos,C., Smyth,K.-A.,
Robin,G.Charlesde.Quetteville., Claudianos,C., Smyth,K.-A.,
Robin,G.Charlesde.Quetteville., Claudianos,C., Smyth,K.-A.,
Boyce,T.Mark., Oakeshott,J.Graham. and Brownlie,J.Colin.
Boyce,T.Mark., Oakeshott,J.Graham. and Brownlie,J.Colin.
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ami nosph	ען די	Insect Biochem. Mol. Biol. 27 (1), 15-25 (1997) 97215578	8799740  2 (bases 1 to 2240)  2 (bases 1 to 2240)  Newcomb.R.D., Campbell, P.M., Russell, R.J. and Oakeshott, J.G. Newcomb. R.D., Campbell, P.M., Russell, R.J. and Oakeshott, J.G. Newcomb. R.D., Campbell, P.M., Russell, R.J. and Oakeshott, J.G. Newcomb. R.D., Campbell, P.M., Russell, R.J. and Oakeshott, J.G. Newcomb. R.D., Campbell, P.M., Russell, R.J. and Oakeshott, J.G. Newcomb. R.D., Campbell, P.M., Russell, R.J. and Oakeshott, J.G. Newcomb. R.D., Campbell, P.M., Russell, R.J. and Oakeshott, J.G. Newcomb. R.D., Campbell, P.M., Russell, R.J. and Oakeshott, J.G. Newcomb. R.D., Campbell, P.M., Russell, R.J. and Oakeshott, J.G. Newcomb. R.D., Campbell, P.M., Russell, R.J. and Oakeshott, J.G. Newcomb. R.D., Campbell, P.M., Russell, R.J. and Oakeshott, J.G. Newcomb. R.D., Campbell, P.M., Russell, R.J. and Oakeshott, J.G. Newcomb. R.D., Campbell, P.M., Russell, R.J. and Oakeshott, J.G. Newcomb. R.D., Campbell, P.M., Russell, R.J. and Oakeshott, J.G. Newcomb. R.D., Campbell, P.M., Russell, R.J. and Oakeshott, J.G. Newcomb. R.D., Campbell, P.M., Russell, R.J. and Oakeshott, J.G. Newcomb. R.D., Campbell, R.D., Russell, R	Newcomb,R.D., East,P.D., Russell,R.J. and Oakeshott,J.G. Isolation of alpha cluster esterase genes associated with organophosphate resistance in Lucilia cuprina Insect Mol. Biol. 5 (3), 211-216 (1996) 96392952	Lucilia cuprina.  SM Lucilia cuprina:  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  Oestroidea; Calliphoridae; Lucilia.  E 1 (bases 1 to 2240)	U56636.1 GI:1336079	LCU56636  1240 bp mRNA linear INV 10-JAN-2002 LCU56636  LUCIlia cuprina alpha esterase (LCaE7) mRNA, implicated in organophosphate resistance complete cds.	TCGATGTTTGAAAAACATAGAGAGATTTATTTAG 1713	TCGATGTTTGAAAAACATAGAGATTTATTTTAG 1713	ATTAGTGACGAAATGAAAATGATTGATGTGCCTGAAATGGATAAGATTAAACAATGGAG 1880 	aaatgtttcctgggatccaattaagaaatccgacgaagtatacaagtgtttgaat 162	ATGGAAAATGTTTCCTGGGATCCAATTAAGAAATCCGATGAAGTATACAAGTGTTTTGAAT 1620	ACTGGTATATGGATACAATTTGCCACCACTGGTAATCCTTATAGCAATGAAATTGAAGGT 1560 	AATCAATTGGCCAAACGTATGCCTAAAGAATCGCGTGAATACAAAACAATTGAACGTATG 1500 	AGTGGACGTGGTGTTAAGGGTGTTAGTCATGCTGATGAATTAACCTATTTCTTCTGG 14	CGTAGTGGACGTGGTGTTAAGGGTGTTAGTCATGCTGATGAATTAACCTATTTCTTCTGG 1440	38	TCTACTTGTATCGCTTCGACTTCGATTCGGAAGATCTTATCAATCCCTATCGTATTATG 138	ω ( 2	_ ~	CATGTTACAGGAGAACACCAACAGCTGATAATTTTATGGATCTTTGCTCTCACATCTAT 1260	

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Campbell, P.M., NewComb, R.D., Russell, R.J. and Oakeshott, J.G.
Two different amino acid substitutions in the ali-esterase, E3,
Two differentive types of organophosphorus insecticide resistance
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proc. Natl. Acad. Sci. U.S.A. 94 (14), 7464-7468 (1997)
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Newcomb, R.D., Campbell, P.M., Russell, R.J. and Oakeshott, J.G.
Direct Submission
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Russell,R.Joyce., Newcomb,R.David., RcBoyce,T.Mark., Campbell,P.Malcolm., PcBoyce,T.Mark., Campbell,P.Malcolm., PcBoxeshott,J.Graham. and Smyth,K.-A. Enzyme based bioremediation
Patent: US 5843758-A 2 01-DEC-1998;
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1 (basea 1 to 2160)
Claudianos, C., Russell, R. J. and Oakeshott, J. G.
The same amino acid substitution in orthologous esterases confers organophosphate resistance on the house fly and a blowfly insect Blochem. Mol. Biol. 29 (8), 675-686 (1999)
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Musca domestica
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Claudianos, C., Rus
Direct Submission
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                        /strain="Rutgers Diazinon-R (R+)"
/db_xref="taxon:7370"
/chromosome="II"
/gene="MdaE7"
         /dev_stage="4 day third instar larvae"
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                                                    /organism="Musca domestica"
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Cloning of a horn fly cDNA, HialphaE7, encoding an esterase whose transcript concentration is elevated in diazinon-resistant flies transect Biochem. Mol. Biol. 30 (11), 1107-1115 (2000)
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Submitted (30-MAR-1999) USDA-ARS,
Insects Research Laboratory, 2700
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Russell,R.Joyce., Newcomb,R.David., Campbell,P.Malcolm., Robin,G.Charlesde,Quetteville., Claudianos,C., Smyth,K.-Boyce,T.Mark., Oakeshott.J.Graham. and Brownlie,J.Colin.Malathion carboxylesterase
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                                                                                                                                                                                                                                      This clone was sequenced as part of a high-throughput process to sequence clones from Drosophila Gene Collection I (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polya tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular cDNA clone. However, there are artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAs, and reverse transcriptase errors that result in single base changes. For further information about this sequence, including its location and relationship to other sequences, please visit our Web site (http://fruitfly.berkeley.edu) or send email to
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Lawrence Berkeley National Laboratory
Berkeley, CA 94720

This clone was sequenced as part of a high-throughput process to sequence clones from Drosophila Gene Collection 1 (Rubin et al., Science 2000). The sequence of a polya tail and contiguity checks for sequence accuracy, presence of a polya tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular cDNA clone. However, there are artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspilced precursor RNAS, and reverse transcriptase errors that result in single base changes.
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Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, USA
Sequence submitted by:
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AY121675
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  For further information about this sequence, including its location and relationship to other sequences, please visit our Web site (http://fruitfly.berkeley.edu) or send email to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             truit
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                                 GGAAACTCCTTCGAAGGTCTCCTCATGTTTCCCGAAGTGAACAAGTGGCCGGAACTGCTT
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                                                                 AACACTTCATATGAGGGTCTATTTTTCACTTCAATTCTTAAGCAAATGCCTATGCTTGTT
                                                                                                                      AAACATCCTCGGGAAATGGTTAAAACTGCTTGGGGTAATTCGATACCCACTATGATGGGT 1038
                                                                                                    AAGTCGCCACTGGAAATGATGCGGGACTGTTGGGGCAACAGCATTCCCATGGTCATCGGA
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Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Metazoa; Arthropoda; Brachycera; Muscomorpha;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

[ (bases 1 to 2820)

Roblin, C., Medveczky, K.M., Russell, R.J. and Oakeshott, J.G.
Roblin, C., Medveczky, K.M., Russell, R.J. and Oakeshott, J.G.
Duplication and Divergence of the genes of the alpha-esterase
Cluster of Drosophila melanogaster
J. Mol. Evol. (1996) In press
Loases 1 to 2820)
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Drosophila melanogaster alpha esterase
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/map="84D3"
/note="Yac c
                                                               /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
                                            /chromosome="3R"
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(aE7) gene,
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                            TTAAAGATCAAGTCATGGCCTTGCGTTGGATTAAAAATAATTGCGCCAACTTTGGTGGCA 622
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CTGCCACGGGTAATCCCTACAGCGAGAAGATCAACGGTATGGACACTCTGACCATTGATC
                                                                                                                CGCCCCAGAGACCTTGGAAATGGGTGCTAAAATTAAAAAGGCTCATGTTACAGGAGAAAC 1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCAGCAGCTTGATGCTGGCACACCTTTCATTCCCAAAGAATTGCTGGCCACGGAGCCCAG
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              CCACCACTGGTAATCCTTATAGCAATGAAATTGAAGGTATGGAAAATGTTTCCTGGGATC
                                                        CGAAGGAAAGTCGCGAACAACAGGAACATCGAACGAACCGTGGGCATCTGGACCCAGTTTG
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                                                                             CTAAAGAATCGCGTGAATACAAAACAATTGAACGTATGACTGGTATATGGATACAATTTG
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AC015272
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This sequence was identified as CDM:10213452 by For further information on this sequence e-mail
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* This sequence will be replaced
* the finished sequence as soon as it is avai
* the accession number will be preserved.
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 57335)
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Muscomorpha;
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to fly@celera.com.
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Search completed: April 11, 2003, 06:06:59 Job time : 3016.03 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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## AAQ91561 RESULT 1 Boyce TM, Campbell PM, Newcomb RD, Oakes Parker AG, Robin GC, Russell RJ, Smyth K; 13-JAN-1994; W09519440-A1 Esterase; E3; bioremediation; organophosphate; carbamate; insecticide; pesticide; water decontamination; meat decontamination; OP-sensitive esterase E3 Lc743 clone. AAQ91561 standard; cDNA; 1713 13-JAN-1995; Lucilia cuprina. 22-DEC-1995 (first entry) (CSIR ) COMMONWEALTH SCI & IND RES ORG 20-JUL-1995 94AU-0003347. 95WO-AU00016 /\*tag= Location/Qualifiers 1..1713 D Oakeshott

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                                                                                                                                                                                                                                                                                                                                                        Pure E3 esterase from Lucilia cuprina and related DNA eliminate residues of organo:phosphate and carbamate per
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AAT68596

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Query Match
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                                                                                          DNA molecule Lc743 (AAT68596) codes for an esterase (AAW17765) from a malathion susceptible strain of Lucilia cuprina. Comparison with a consensus sequence from derived from clones of the Lc-alpha-E7 resistant allele (see also AAW17768) indicated only one replacement site difference, a Trp to Leu substitution at amino acid position 251 (nucleotide position 752). This mutation is an excellent candidate for the malathion resistance mutation. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mutation
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                                                                                                                                                                                                                DNA encoding enzyme that degrades organophosphate pesticides useful for decontamination of soil, water, food etc
                                                                                                                                                                                                                                                                                                                                                  23-NOV-1995;
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                                    Sequence 1713 BP;
                                                                    excellent candidate for the malathion resistance mutation. The resistant enzyme acts as a malathion carboxylesterase and can be formulated for use in degrading environmental carboxylester or
                                                                                                                                                                                                                                                      WPI; 1997-298113/27
P-PSDB; AAW17765.
                                                                                                                                                                                                                                                                                          Newcomb
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                                                                                                                                                                                                                                                                                                                          (CSIR ) COMMONWEALTH SCI & IND RES ORG.
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                                                         general organophosphates
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D, Oakeshott
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remediation; bioremediation; decontamination;
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                                  516 A; 305 C; 370 G; 522 T; 0 other;
99.4%;
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JG, Robin GC,
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"base 1629 is T in resistant clones
(silent mutation)"
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(silent mutation)"
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(silent mutation)"
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Score 1703.4;
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Russell RJ,
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                                                                                           op-resistant
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          13-JAN-1995;
                               WO9519440-A1
                                                             Lucilia
 13-JAN-1994;
                    20-JUL-1995
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TTCTGGTTCCCCATGCATCGTTTGTTGCAATTACGTTTCAATCACACCTCCGGTACACCC
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            95WO-AU00016
                                              Location/Qualifiers
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Matches 1694; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pure E3 esterase from Lucilia cuprina and eliminate residues of organo:phosphate and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  water, meat etc.
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1713 BP;
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Robin GC, R
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nilarity 98.9%;
Conservative (
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Russell RJ,
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d carbamate pes
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
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eliminate residues
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ATAACGGGCAAAGTGTGTGGCTCAGAGGGATTGTCTATACCTAAGTGTCTATACGAATAAT
                                 CCCTGGGATGGTGTGCGTGATTGTTGCAATCATAAAGATAAGTCAGTGCAAGTTGATTTT
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                         CCCTGGGATGGTGTGCGTGATTGTTGCAATCATAAAGATAAGTCAGTGCAAGTTGATTTT
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Robin GC, R
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pesticide; water decontamination;
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                                                   RT-PCR was used to clone a cDNA allele of Lc-alpha-E7 (encoding op-susceptible esterase E3 of L. cuprina) from a diazinon resistant strain, Llandillo 103. 4 Isolated clones were sequenced (Lc/Ll03 A-D, AAQ91562-65) that encoded diazinin-resistant esterases. The esterases, or cells expressing them, are used
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insecticide; p
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Robin GC, R
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pesticide; water decontamination;
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insecticide;
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                                                                                 pesticide;
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pesticide; water
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Parker AG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pure E3 esterase from Lucilia cuprina and related DNA - used to eliminate residues of organo:phosphate and carbamate pesticides
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in bioremediation.
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Robin GC, R
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Russell RJ, Smyth K;
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Robin GC, R
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A 1710 bp DNA molecule (AAT68597) comprises the Md-alpha-E7 coding sequence of the Musca domestica Rutgers strain. It was isolated by amplification of genomic DNA using alpha-esterase consensus primers (see also AAT68598-99) and use of a 534 bp amplicon to screen a genomic library of M. domestica. A mutation of the gene, resulting in substr. of serine for tryptophan at amino acid position 251 (see also AAM17767), confers malathion
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23-MAR-2000;
11-JUL-2000;
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                                                             WO200171042-A2
                                                                              Drosophila melanogaster
                                                                                                                          Drosophila melanogaster expressed
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2000US-0614150
                          2001WO-US09231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic a genes from Drosophila interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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The sequence data for this patent did not form specification, but was obtained in electronic i at ftp.wipo.int/pub/published\_pct\_sequences.

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                          TCAAGGATCAGGTGCTGGCCCTCAAGTGGATCAAGAACAATTGCGCTAGTTTCGGCGGAG
                                                                                                  TTTGTCCATTGGC---TAATACCCAATGTCAACATCGTGCCTTCACCTTAGCCAAATTGG
                                                                                                             TGTTAACCGAACAAACTCGCGGTCTTTTCCATCGTGGTATACTAATGTCGGGTAATGCTA 742
CACAGGATTTAATAAAACTTGAGGAAAAAGTTTTAACTCTAGAAGAGGGGTACAAATAAGG 919
                                                               TTTGTCCTTGGGCCTACAACGGCGACATTACCCATAATCCCTACAGGATAGCCAAGCTGG
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illarity 54.5%;
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pred. No. 2.2e-91;
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                                                                                           CAATTAAGAAATCCGATGAAGTATACAAGTGTTTGAATATTAGTGATGAATTGAAAATGA 1642
                                                                                                                                                       CCACCACTGGTAATCCTTATAGCAATGAAATTGAAGGTATGGAAAATGTTTCCTGGGATC
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                                             TCGATCTGCCTGAGTGGCCCAAATTGAAGGTCTGGGAGAGCCTCTATGACGACAACAAAG
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                                                                                                                                                                                                                                                                                                                                                                                 The sequence data for this patent did not form part of the pri
specification, but was obtained in electronic format directly
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                    TTGAAAATAAGTTTTTAAACTATCGTTTAACTACCAATGAAACGGTGGTAGCTGAAACTG
CAAAGAATTTGTATCCCACCAAACCAATGCCCGTGATGGTCTGGATCTATGGCGGTGGCT
                                                          TTGATTTTATAACGGGCAAAGTGTGTGTGGCTCAGAGGATTGTCTATACCTAAGTGTCTATA
                                                                                                CCCCGGAGGTCTGGACGGAGGTCAGGAGCTGCACCTCCCAGGGTCCCAAGCCACTGCAGA
                                                                                                                      GACCAACACCCTGGGATGGTGCGTGATTGTTGCAATCATAAAGATAAGTCAGTGCAAG
                                                                                                                                                TCGAGCGGATCCCCTTCGCCAAACCACCGGTGGGCGAGCTACGCTACAAGGCTCCCCAGC
                                                                                                                                                          TTGAGGGTATACCCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCACCCCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster
                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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11-JUL-2000;
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P-PSDB; ABB60586.
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                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 8549; 21pp + Sequence Listing; English.
                                                                                                                                                             The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                        interactions
                                                                                                                              Sequence 1792
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                                                    Local Similarity 53.0 (es 861; Conservative
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                                                                                    CAATTCTTAAGCAAATGCCTATGCTTGATGAGGAATTGGAAACTTGTGTCAATTTTGTGC 1129
                                                                                                                                                    GGGGTAATTCGATACCCACTATGATGGGTAACACTTCATATGAGGGTCTATTTTCACTT 1069
                                                                                                                                                                                                                            CATATCAGACCGCTGATTGTGTCTTACCCAAACATCCTCGGGAAATGGTTAAAACTGCTT 1009
                                                                                                                                 GGGGCAACGACATTCCCGTTATTGTCGGTGGAAATTCTTTCGAGGGCTTGTTTTCCTACC 1163
                                CAAGTGAATTGGCTGATGCTGAACGCACCGCCCCAGAGACCTTGGAAATGGGTGCTAAAA 1189
                                                                 AACTAGTAAGAAAAGATCCTTGGGCCTTGAAAAACTTTCACAACATCCTGCCAAGGGAGG
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                                                                                                                New isolated nucleic acid genes from Drosophila and interactions -
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABL02103;
The invention relates to an isolated nucleic capable of detecting 1000 or more genes from
                                                                      Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAR-2001;
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DB; ABB58000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid genes from Drosophila and interactions .
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P-PSDB; ABB57756.
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11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
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Search completed: April 11, 2003, 01:06:53 Job time: 263.905 secs

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Maximum Match 100%
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A1388926 GH19977.5
A1403569 GH23036.5
A1517692 GH28740.5
B1609541 RH14337.5
B1628316 RH56682.5
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## ALIGNMENTS

FEATURES	AUTHORS TITLE JOURNAL COMMENT	KEYWORDS SOURCE ORGANISM	RESULT 1 A1062034 LOCUS DEFINITION ACCESSION VERSION
Lawrence Berkeley National Lab One Cyclotron Rd, Berkeley, CA 94720, USA Fax: 510 486 6798 Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu Plate: 10 row: G column: 4 High quality sequence stop: 363. Location/Qualifiers	1 (Dases 1 to 70) Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G., Lewis,S. and Rubin,G.M. BDGP/HHMI Drosophila EST Project Unpublished (2001) Contact: Stapleton, M.	EST. fruit fly. fruit fly. Drosophila melanogaster Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.	AI062034 778 bp mRNA linear EST 19-APR-2001 GH01076.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH01076 5prime similar to U51050: ; Drosophila melanogaster alpha esterase (aE7) gene, partial cds, aI062034.1 GI:3337873

Su, C., Tsang

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| GGCGCCTCCACTCACTACATGATGCTAA 778
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AI388926 649 bp mRNA linear EST 19-APR-GH19977.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH19977 5prime similar to U51050: Drosophila melanogaster alpha esterase (aE7) gene, partial cds.
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Pred. No. 1e-74;
0; Mismatches 234;
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422; Conserv
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Eukaryota; Metazoa; Arthropoda; Brachycera;
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 649)
                                                                              TGAAAGCCAAGCCACAGGATTTAATAAAACTTGAGGAAAAAGTTTTAACTCTAGAAGAGC 907
                                                                                                                                                       TAGCCAAGCTGGTTGGCTACAAGGGCGAGGACAACGACAAGGATGTGCTGGAGTTCTTGC
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Lewis, S. and Rubin, G.M.
BDGP/HHMI Drosophila EST
Unpublished (2001)
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A1388926
                                                      Email: http://www.fruitfly.org/EST, plate: 199 row: G column: 5
High quality sequence stop: 559.
Location/Qualifiers
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One Cyclotron Rd,
Fax: 510 486 6798
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pred. No. 3.4e-66;
0; Mismatches 211;
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                                                          AAAGTGAAAGGCGTTAAACGTTTAACTGTGTGCTACGATGATTCCTACTACTACTGTTTTGAGGGT
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                                                                                                          ANAGTCCAGCAGTATCGCCAGTCGACCAATGAAACAGTTGTCGCCGACACGGAGTACGGC
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1 (bases 1 to 688)
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One Cyclotron Rd, Berkeley, CA 94720,
Fax: 510 486 6798
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BDGP/HHMI Drosophila EST Project
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/dev_stage="adult"
/lab_host="DH5 - alpha"
/note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
XhoI; Sized fractionated cDNAs were directly ligated into
pOT2. Plasmid cDNA library."
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/db_xref="taxon:7227"
/clone="GH23036"
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BDGP/HHMI Drosophila EST Project
Unpublished (2001)
Contact: Stapleton, M.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 671)
                                                                                                                                                                                                                                                                                                                             Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA
Fax: 510 486 6798
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/lab_host="DH5 - alpha"
/lab_host="DH5 - alpha"
/note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
/note="Organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
XhoI; Sized fractionated cDNAs were directly ligated into
pOT2._ Plasmid_cDNA library."
                                                                                                                                                                       /organism="Drosophila
/db_xref="taxon:7227"
/clone="GH28740"
                                                                                                                                 /clone_lib="GH Drosophila melanogaster
/sex="male and female"
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Query Match Best Local Similarity

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Score 256.6; DB 9; Pred. No. 3.9e-59;

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                                                                                                                                                               Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Lidao, G., Misra, S., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and Rubin, G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B1609541 linear EST 07-SEP-2001 RH14337.5prime RH Drosophila melanogaster normalized Head pFlc-1 Drosophila melanogaster cDNA clone RH14337.5 similar to alpha-Est7: FBan0001112 GO:[carboxyesterase (GO:0004091); carboxyesterase (GO:0004091)] located on: 3R 84D5-84D5;: 08/17/2001, mRNA sequence.
                                                                                                                                                                                                                                                                                                           prosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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EST.
                                                                                                                       BDGP/HHMI RH Drosophila EST Unpublished (2001)
           Lawrence Berkeley
One Cyclotron Rd,
Fax: 510 486 6798
                                                                             Contact: Stapleton, BDGP
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est@fruitfly.berkeley
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'dev_scage="Adult"

/lab_host="pH5-alpha TonA"

/note="Organ: head; Vector: pFlc1; Site_1: xhoI; Site_2:

/note="Organ: head; Vector by Plero Carninci at the RIKEN. The library was normalized and excised using the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library."

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/db_xref="taxon:7227"
/clone="RH14337"
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                                                                          CAAGTGAGGGGTATCAAGCGTCTATCTCTCTACGATGTGCCCTACTTCAGCTTCGAGGGT
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                                     GTGAAGCCCGACAAGGCTCGCCCGGTTATGGTTTGGATTCACGGAGGAGGCTTCATTATC
                                                                                                               GTCTTCGATAAGGTAGAGGGCTCCGAGGACTGCCTCTATCTCAATGTGTACACCAACAAT
                                                                                                                                  ATAACGGGCAAAGTGTGTGGCTCAGAGGATTGTCTATACCTAAGTGTCTATACGAATAAT
                                                                                                                                                                                                                        CCCTGGGATGGTGCGTGATTGTTGCAATCATAAAGATAAGTCAGTGCAAGTTGATTTT
                                                                                                                                                                                                                                                                 ATCCCGTACGCCCAGCCTCCGGTGGGGGGAGTTGCGGTTTAAGGCCCCCTCAGAGGCCCCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGAATAAGAACCTCGGCTTTGTGGAGCGCCTTGCGGTGGCGCCTCAAAACCATCGAGCAT
 GGTGAAAATCATCGTGATATGTATGGTCCTGATTATTTCATTAAAAAAGGATGTGGTGTTG
                                                                                                                                                                                     CCCTGGGAGCGAGTTCGCGACTGCAGCCGAGCCGAAGGATAAGGCCGTCCAGGTGCAGTTC
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Contact: Stapleton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Misra, S., Mungall, C.J., Nunco, J., Pacleb, J., Paragas, V., Park, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and Rubin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 674)
Stapleton, M., Brokstein, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Neoptera; Endopterygota; Diptera; Brachycera; Musco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: http://www.fruitfly.org/EST, Plate: RH.566 row: G column: 10 High quality sequence stop: 558.
Location/Qualifiers
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/note="Organ: head; Vector: pFlc1; Site_1: XhoI; Site_2:
/note="Organ: head; Vector: pFlc1; Site_1: XhoI; Site_2:
BamHI; Library was kindly generated by Piero Carninci at
the RIKEN. The library was normalized and excised using
Cre recombinase. Plasmid cDNA library."
170 c 195 g 155 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="RH56682"
/clone_lib="RH Drosophila melanogaster normalized
pp[c-1"
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ATACCGTACGCCCAACCGCCAGTGGGTGAGCTGAGATTTAAAGCACCCCAGCGACCAACA
                                                                                                                                        AAGTTTTTAAACTATCGTTTAACTACCAATGAAACGGTGGTAGCTGAAACTGAATATGGC 120
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                                                                                   AAAGTGAAAGGCGTTAAACGTTTAACTGTGTACGATGATTCCTACTACAGTTTTGAGGGT
                                                                                                                                                                                     ATGAATAAGAACCTCGGCTTTGTGGAGCGCCTTGCGGTGGCGCCTCAAAACCATCGAGCAT 173
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                                                                                                                                                                                                                                                        367;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: http://www.fruitfly.org/EST, Plate: SD.167 row: A column: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               One Cyclotron Rd, Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lawrence Berkeley National Lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2001)
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Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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173 c 194 g 154 t
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/db_xref="taxon:7227"
/clone="SD16705"
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Pred. No. 3.7e-57;
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390; Conserv
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Lewis, S. and Rubin, G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                BDGP/HHMI RH Drosophila
Unpublished (2001)
Contact: Stapleton, M.
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BI614443 672 bp mRNA linear EST 07-SEP-2001 RH43812.5prime RH Drosophila melanogaster cDNA clone RH43812.5 similar to alpha-Est7: FBan0001112 GO:[carboxyesterase (GO:0004091); carboxyesterase
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/Sex="male and female"
/dev_stage="Adult"
/lab_host="DH5-alpha TonA"
/note="Organ: head; Vector: pFlc1; Site_1: XhoI; Site_2:
BanHI; Library was kindly generated by Piero Carninci at
the RIKEN. The library was normalized and excised using
Cre recombinase. Plasmid cDNA library "
a 169 c 195 g 155 t 1 others
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/db_xref="taxon:7227"
/clone="RH43493"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lawrence Berkeley National One Cyclotron Rd, Berkeley, Fax: 510 486 6798
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EST.
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BDGP/HHMI RH Drosophila EST Project Unpublished (2001)
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/db_xref="taxon:7227"
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AAGTTTTTAAACTATCGTTTAACTACCAATGAAACGGTGGTAGCTGAAACTGAATATGGC
                                                                           ATGAATAAGAACCTCGGCTTTGTGGAGCGCTTGCGGTGGCGCCTCAAAACCATCGAGCAT 169
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Eukaryota; Brachycera;
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila:
1 (bases 1 to 670)
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Email: http://www.fruitfly.org/EST,
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One Cyclotron Rd, Berkeley, CA 94720, USA
                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                         152
                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                 /note="Organ: embryo; Vector: pFlc1; Site_1: XhoI; Site_1: BamHI; Library was kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library."

168 c 194 g 155 t l others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="RE29491"
                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="male and female"
/dev_stage="0-24 hours mixed stage embryonic"
/lab_host="DH5-alpha TonA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="RE Drosophila melanogaster normalized
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                                                                                                                                                                                                                                                                                                                                                                  Harvey,D., Brokstein,P., Hong,L.,
Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 648)
Harvoy n Broketein D Honn I. France-Holm.M Sn C Teanor
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AI113763.1 GI:3514566
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plate: 102 row: B column: 1
High quality sequence stop: 435.
Location/Qualiflers
                                                                                                                                                                                                                                                                 One Cyclotron Rd, Fax: 510 486 6798
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                                                                                                                                                                                                                                                                                                           Lawrence Berkeley
                                                                                             /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="6H10213"
             /Clone_lib="GH Drosophila
/sex="male and female"
/dev_stage="adult"
/lab_host="DH5 - alpha"
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